

SEQUENCE LISTING

<110> Croteau, Rodney B
Bohlmann, Joerg
Steele, Christopher L
Phillips, Michael A

<120> MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)

<130> WSUR18414

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<150> 09/360,545
<151> 1999-07-26

<150> 60/052,249
<151> 1997-07-11

<150> PCT/US98/14528
<151> 1998-07-10

<160> 107

<170> PatentIn Ver. 2.0

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<222> (69)..(1952)
<223> Clone AG2.2 encoding myrcene synthase

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Leu Arg Lys Ser Leu Ile Ser Ser Ile His Glu His Lys Pro Pro Tyr
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Arg Thr Ile Pro Asn Leu Gly Met Arg Arg Gly Lys Ser Val Thr
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Pro Ser Met Ser Ile Ser Leu Ala Thr Ala Ala Pro Asp Asp Gly Val
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Ser Thr Ala Leu Gly Phe Arg Thr Leu Arg Leu His Gly Tyr Thr Val			
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Ser Pro Glu Val Leu Lys Ala Phe Gln Asp Gln Asn Gly Gln Phe Val			
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Tyr Arg Ala Ser Leu Ile Ala Phe Pro Gly Glu Lys Val Met Glu Glu			
225	230	235	
gct gaa atc ttc tcc aca aga tat ttg aaa gaa gct cta caa aag att			830
Ala Glu Ile Phe Ser Thr Arg Tyr Leu Lys Glu Ala Leu Gln Lys Ile			
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Pro Val Ser Ala Leu Ser Gln Glu Ile Lys Phe Val Met Glu Tyr Gly			
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tgg cac aca aat ttg cca aga ttg gaa gca aga aat tac ata gac aca			926
Trp His Thr Asn Leu Pro Arg Leu Glu Ala Arg Asn Tyr Ile Asp Thr			
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Leu Glu Lys Asp Thr Ser Ala Trp Leu Asn Lys Asn Ala Gly Lys Lys			
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Leu Leu Glu Leu Ala Lys Leu Glu Phe Asn Ile Phe Asn Ser Leu Gln			
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aga tgg aat tca tca gag ata gaa cac ctt cca gaa tat atg aaa tgt Arg Trp Asn Ser Ser Glu Ile Glu His Leu Pro Glu Tyr Met Lys Cys 400 405 410			1310
gtg tac atg gtc gtg ttt gaa act gta aat gaa ctg aca cga gag gcg Val Tyr Met Val Val Phe Glu Thr Val Asn Glu Leu Thr Arg Glu Ala 415 420 425 430			1358
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atc aat gcc atg gtc aat gac ata atc aaa gaa tta aat tgg gaa ctt Ile Asn Ala Met Val Asn Asp Ile Ile Lys Glu Leu Asn Trp Glu Leu 560 565 570			1790

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Leu Arg Ser Asn Asp Asn Ile Pro Met Leu Ala Lys Lys His Ala Phe
575 580 585 590

gac ata aca aca gct ctc cac cat ctc tac ata tat cga gat ggc ttt 1886
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595 600 605

agt gtt gcc aac aag gaa aca aaa aaa ttg gtt atg gaa aca ctc ctt 1934
Ser Val Ala Asn Lys Glu Thr Lys Lys Leu Val Met Glu Thr Leu Leu
610 615 620

gaa tct atg ctt ttt taa ctataaccat atccataata ataagctcat 1982
Glu Ser Met Leu Phe
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Arg Ile Gly Asp Tyr His Ser Asn Ile Trp Asp Asp Asp Phe Ile Gln
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Arg Leu Ile Val Glu Val Lys Lys Ile Phe Asn Ser Met Tyr Leu Asp
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115 120 125

Ile Val Asp Ser Val Glu Arg Leu Gly Ile Ala Arg His Phe Lys Asn
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Pro Gly Gln Thr Glu Gly Glu Ile Arg Ser Val Leu Asn Leu Tyr Arg
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Glu Leu Gln Tyr Leu Leu Arg Trp Trp Lys Glu Ser Asp Leu Pro Lys
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Leu Thr Phe Ala Arg His Arg His Val Glu Phe Tyr Thr Leu Ala Ser
340 345 350

Cys Ile Ala Ile Asp Pro Lys His Ser Ala Phe Arg Leu Gly Phe Ala
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Lys Met Cys His Leu Val Thr Val Leu Asp Asp Ile Tyr Asp Thr Phe
370 375 380

Gly Thr Ile Asp Glu Leu Glu Leu Phe Thr Ser Ala Ile Lys Arg Trp
385 390 395 400

Asn Ser Ser Glu Ile Glu His Leu Pro Glu Tyr Met Lys Cys Val Tyr
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Pro Asp Tyr Ile Leu Lys Gly Ile Asp Phe Pro Ser Arg Phe Asn Asp
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Leu Ala Ser Ser Phe Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys
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Ser Asn Asp Asn Ile Pro Met Leu Ala Lys Lys His Ala Phe Asp Ile
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Thr Arg Ala Leu His His Leu Tyr Ile Tyr Arg Asp Gly Phe Ser Val
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His Lys Ser Leu Ile Ser Ser Thr His Glu Leu Lys Ala Leu Ser Arg
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aca att cca gct cta gga atg agt agg cga ggg aaa tct atc act cct 146
Thr Ile Pro Ala Leu Gly Met Ser Arg Arg Gly Lys Ser Ile Thr Pro
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Ser Ile Ser Met Ser Ser Thr Thr Val Val Thr Asp Asp Gly Val Arg
50 55 60

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gaa gat gga gag tta atg agt ccg ctc aat gat ctc att caa cgc ctt		386
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Asp Glu Ile Lys Ser Ala Leu Asp Tyr Val Tyr Ser Tyr Trp Gly Glu		
145	150	155
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Asn Gly Ile Gly Cys Gly Arg Glu Ser Val Val Thr Asp Leu Asn Ser		
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225	230	235
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Ala Glu Ile Phe Ser Thr Lys Tyr Leu Lys Glu Ala Leu Gln Lys Ile		
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Pro Val Ser Ser Leu Ser Arg Glu Ile Gly Asp Val Leu Glu Tyr Gly		
260	265	270
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Trp His Thr Tyr Leu Pro Arg Leu Glu Ala Arg Asn Tyr Ile Gln Val		
275	280	285
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Phe Gly Gln Asp Thr Glu Asn Thr Lys Ser Tyr Val Lys Ser Lys Lys		
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Leu Leu Glu Leu Ala Lys Leu Glu Phe Asn Ile Phe Gln Ser Leu Gln		
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Pro Glu Met Thr Phe Cys Arg His Arg His Val Glu Tyr Tyr Thr Leu
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385 390 395

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Arg Trp Asp Pro Ser Ser Ile Asp Cys Leu Pro Glu Tyr Met Lys Gly
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420 425 430

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Glu Glu Ala Gln Gly Arg Asp Thr Leu Thr Tyr Ala Arg Glu Ala Trp
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Glu Ala Tyr Ile Asp Ser Tyr Met Gln Glu Ala Arg Trp Ile Ala Thr
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Gly Tyr Leu Pro Ser Phe Asp Glu Tyr Tyr Glu Asn Gly Lys Val Ser
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Cys Gly His Arg Ile Ser Ala Leu Gln Pro Ile Leu Thr Met Asp Ile
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Pro Phe Pro Asp His Ile Leu Lys Glu Val Asp Phe Pro Ser Lys Leu
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Asn Asp Leu Ala Cys Ala Ile Leu Arg Leu Arg Gly Asp Thr Arg Cys
515 520 525

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Tyr Lys Ala Asp Arg Ala Arg Gly Glu Glu Ala Ser Ser Ile Ser Cys
530 535 540

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Tyr Met Lys Asp Asn Pro Gly Val Ser Glu Glu Asp Ala Leu Asp His
545 550 555

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Ile Asn Ala Met Ile Ser Asp Val Ile Lys Gly Leu Asn Trp Glu Leu
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Asp Ile Ala Arg Ala Phe His Tyr Gly Tyr Lys Tyr Arg Asp Gly Tyr
595 600 605

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Glu Ser Val Pro Leu
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Arg Met Gly Asp Phe His Ser Asn Leu Trp Asp Asp Asp Val Ile Gln
65 70 75 80

Ser Leu Pro Thr Ala Tyr Glu Glu Lys Ser Tyr Leu Glu Arg Ala Glu
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Lys Leu Ile Gly Glu Val Lys Asn Met Phe Asn Ser Met Ser Leu Glu
100 105 110

Asp Gly Glu Leu Met Ser Pro Leu Asn Asp Leu Ile Gln Arg Leu Trp
115 120 125

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245	250	255
Val Ser Ser Leu Ser Arg Glu Ile Gly Asp Val Leu Glu Tyr Gly Trp		
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Ala Lys Thr Cys His Leu Ile Thr Val Leu Asp Asp Met Tyr Asp Thr		
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Phe Gly Thr Val Asp Glu Leu Glu Leu Phe Thr Ala Thr Met Lys Arg		
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Ala Tyr Ile Asp Ser Tyr Met Gln Glu Ala Arg Trp Ile Ala Thr Gly		
450	455	460
Tyr Leu Pro Ser Phe Asp Glu Tyr Tyr Glu Asn Gly Lys Val Ser Cys		
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Lys Ala Asp Arg Ala Arg Gly Glu Glu Ala Ser Ser Ile Ser Cys Tyr
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Met Lys Asp Asn Pro Gly Val Ser Glu Glu Asp Ala Leu Asp His Ile
545 550 555 560

Asn Ala Met Ile Ser Asp Val Ile Lys Gly Leu Asn Trp Glu Leu Leu
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Lys Pro Asp Ile Asn Val Pro Ile Ser Ala Lys Lys His Ala Phe Asp
580 585 590

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Ser Val Pro Leu
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Met Ala Leu Leu Ser Ile Val Ser Leu Gln Val Pro Lys
1 5 10

tcc tgc ggg ctg aaa tcg ttg atc agt tcc agc aat gtg cag aag gct 159
Ser Cys Gly Leu Lys Ser Leu Ile Ser Ser Asn Val Gln Lys Ala
15 20 25

ctc tgt atc tct aca gca gtc cca aca ctc aga atg cgt agg cga cag 207
Leu Cys Ile Ser Thr Ala Val Pro Thr Leu Arg Met Arg Arg Arg Gln
30 35 40 45

aaa gct ctg gtc atc aac atg aaa ttg acc act gta tcc cat cgt gat 255
Lys Ala Leu Val Ile Asn Met Lys Leu Thr Thr Val Ser His Arg Asp
50 55 60

gat aat ggt ggt ggt gta ctg caa aga cgc ata gcc gat cat cat ccc 303
Asp Asn Gly Gly Val Leu Gln Arg Arg Ile Ala Asp His His Pro
65 70 75

aac ctg tgg gaa gat gat ttc ata caa tca ttg tcc tca cct tat ggg 351
Asn Leu Trp Glu Asp Asp Phe Ile Gln Ser Leu Ser Ser Pro Tyr Gly
80 85 90

gga tct tcg tac agt gaa cgt gct gag aca gtc gtt gag gaa gta aaa 399
Gly Ser Ser Tyr Ser Glu Arg Ala Glu Thr Val Val Glu Glu Val Lys
95 100 105

gag atg ttc aat tca ata cca aat aat aga gaa tta ttt ggt tcc caa 447
Glu Met Phe Asn Ser Ile Pro Asn Asn Arg Glu Leu Phe Gly Ser Gln
110 115 120 125

aat gat ctc ctt aca cgc ctt tgg atg gtg gat agc att gaa cgt ctg 495
Asn Asp Leu Leu Thr Arg Leu Trp Met Val Asp Ser Ile Glu Arg Leu
130 135 140

ggg ata gat aga cat ttc caa aat gag ata aga gta gcc ctc gat tat 543
Gly Ile Asp Arg His Phe Gln Asn Glu Ile Arg Val Ala Leu Asp Tyr
145 150 155

gtt tac agt tat tgg aag gaa aag gaa ggc att ggg tgt ggc aga gat 591
Val Tyr Ser Tyr Trp Lys Glu Lys Glu Gly Ile Gly Cys Gly Arg Asp
160 165 170

tct act ttt cct gat ctc aac tcg act gcc ttg gcg ctt cga act ctt 639
Ser Thr Phe Pro Asp Leu Asn Ser Thr Ala Leu Ala Leu Arg Thr Leu
175 180 185

cga ctg cac gga tac aat gtg tct tca gat gtg ctg gaa tac ttc aaa 687
Arg Leu His Gly Tyr Asn Val Ser Ser Asp Val Leu Glu Tyr Phe Lys
190 195 200 205

gat gaa aag ggg cat ttt gcc tgc cct gca atc cta acc gag gga cag 735
Asp Glu Lys Gly His Phe Ala Cys Pro Ala Ile Leu Thr Glu Gly Gln
210 215 220

atc act aga agt gtt cta aat tta tat cgg gct tcc ctg gtc gcc ttt 783
Ile Thr Arg Ser Val Leu Asn Leu Tyr Arg Ala Ser Leu Val Ala Phe
225 230 235

ccc ggg gag aaa gtt atg gaa gag gct gaa atc ttc tcg gca tct tat 831
Pro Gly Glu Lys Val Met Glu Ala Glu Ile Phe Ser Ala Ser Tyr
240 245 250

ttg aaa aaa gtc tta caa aag att ccg gtc tcc aat ctt tca gga gag 879
Leu Lys Lys Val Leu Gln Lys Ile Pro Val Ser Asn Leu Ser Gly Glu
255 260 265

ata gaa tat gtt ttg gaa tat ggt tgg cac acg aat ttg ccg aga ttg 927
Ile Glu Tyr Val Leu Glu Tyr Gly Trp His Thr Asn Leu Pro Arg Leu
270 275 280 285

gaa gca aga aat tat atc gag gtc tac gag cag agc ggc tat gaa agc 975
Glu Ala Arg Asn Tyr Ile Glu Val Tyr Glu Gln Ser Gly Tyr Glu Ser
290 295 300

tta aac gag atg cca tat atg aac atg aag aag ctt tta caa ctt gca 1023
Leu Asn Glu Met Pro Tyr Met Asn Met Lys Lys Leu Leu Gln Leu Ala
305 310 315

aaa ttg gag ttc aat atc ttt cac tct ttg caa cta aga gag tta caa Lys Leu Glu Phe Asn Ile Phe His Ser Leu Gln Leu Arg Glu Leu Gln 320 325 330	1071
tct atc tcc aga tgg tgg aaa gaa tca ggt tcg tct caa ctg act ttt Ser Ile Ser Arg Trp Trp Lys Glu Ser Gly Ser Ser Gln Leu Thr Phe 335 340 345	1119
aca cgg cat cgt cac gtg gaa tac tac act atg gca tct tgc att tct Thr Arg His Arg His Val Glu Tyr Tyr Thr Met Ala Ser Cys Ile Ser 350 355 360 365	1167
atg ttg cca aaa cat tca gct ttc aga atg gag ttt gtc aaa gtg tgt Met Leu Pro Lys His Ser Ala Phe Arg Met Glu Phe Val Lys Val Cys 370 375 380	1215
cat ctt gta aca gtt ctc gat gat ata tat gac act ttt gga aca atg His Leu Val Thr Val Leu Asp Asp Ile Tyr Asp Thr Phe Gly Thr Met 385 390 395	1263
aac gaa ctc caa ctt ttt acg gat gca att aag aga tgg gat ttg tca Asn Glu Leu Gln Leu Phe Thr Asp Ala Ile Lys Arg Trp Asp Leu Ser 400 405 410	1311
acg aca agg tgg ctt cca gaa tat atg aaa gga gtg tac atg gac ttg Thr Thr Arg Trp Leu Pro Glu Tyr Met Lys Gly Val Tyr Met Asp Leu 415 420 425	1359
tat caa tgc att aat gaa atg gtg gaa gag gct gag aag act caa ggc Tyr Gln Cys Ile Asn Glu Met Val Glu Ala Glu Lys Thr Gln Gly 430 435 440 445	1407
cga gat atg ctc aac tat att caa aat gct tgg gaa gcc cta ttt gat Arg Asp Met Leu Asn Tyr Ile Gln Asn Ala Trp Glu Ala Leu Phe Asp 450 455 460	1455
acc ttt atg caa gaa gca aag tgg atc tcc agc agt tat ctc cca acg Thr Phe Met Gln Glu Ala Lys Trp Ile Ser Ser Tyr Leu Pro Thr 465 470 475	1503
ttt gag gag tac ttg aag aat gca aaa gtt agt tct ggt tct cgc ata Phe Glu Glu Tyr Leu Lys Asn Ala Lys Val Ser Ser Gly Ser Arg Ile 480 485 490	1551
gcc aca tta caa ccc att ctc act ttg gat gta cca ctt cct gat tac Ala Thr Leu Gln Pro Ile Leu Thr Leu Asp Val Pro Leu Pro Asp Tyr 495 500 505	1599
ata ctg caa gaa att gat tat cca tcc aga ttc aat gag tta gct tcg Ile Leu Gln Glu Ile Asp Tyr Pro Ser Arg Phe Asn Glu Leu Ala Ser 510 515 520 525	1647
tcc atc ctt cga cta cga ggt gac acg cgc tgc tac aag gcg gat agg Ser Ile Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys Ala Asp Arg 530 535 540	1695
gcc cgt gga gaa gaa gct tca gct ata tcg tgt tat atg aaa gac cat Ala Arg Gly Glu Glu Ala Ser Ala Ile Ser Cys Tyr Met Lys Asp His 545 550 555	1743
cct gga tca ata gag gaa gat gct ctc aat cat atc aac gcc atg atc	1791

Pro Gly Ser Ile Glu Glu Asp Ala Leu Asn His Ile Asn Ala Met Ile
560 565 570

agt gat gca atc aga gaa tta aat tgg gag ctt ctc aga ccg gat agc 1839
Ser Asp Ala Ile Arg Glu Leu Asn Trp Glu Leu Leu Arg Pro Asp Ser
575 580 585

aaa agt ccc atc tct tcc aag aaa cat gct ttt gac atc acc aga gct 1887
Lys Ser Pro Ile Ser Ser Lys Lys His Ala Phe Asp Ile Thr Arg Ala
590 595 600 605

ttc cat cat gtc tac aaa tat cga gat ggt tac act gtt tcc aac aac 1935
Phe His His Val Tyr Lys Tyr Arg Asp Gly Tyr Thr Val Ser Asn Asn
610 615 620

gaa aca aag aat ttg gtg atg aaa acc gtt ctt gaa cct ctc gct ttg 1983
Glu Thr Lys Asn Leu Val Met Lys Thr Val Leu Glu Pro Leu Ala Leu
625 630 635

taa aaacatatacg aatgcattaa aatgtggaa gtctataatc tagactattc 2036

tctatcttc ataatgtaga tctggatgtg tattgaactc taaaaaaaaaaa aaa 2089

<210> 6
<211> 637
<212> PRT
<213> Abies grandis

<400> 6
Met Ala Leu Leu Ser Ile Val Ser Leu Gln Val Pro Lys Ser Cys Gly
1 5 10 15

Leu Lys Ser Leu Ile Ser Ser Ser Asn Val Gln Lys Ala Leu Cys Ile
20 25 30

Ser Thr Ala Val Pro Thr Leu Arg Met Arg Arg Arg Gln Lys Ala Leu
35 40 45

Val Ile Asn Met Lys Leu Thr Thr Val Ser His Arg Asp Asp Asn Gly
50 55 60

Gly Gly Val Leu Gln Arg Arg Ile Ala Asp His His Pro Asn Leu Trp
65 70 75 80

Glu Asp Asp Phe Ile Gln Ser Leu Ser Ser Pro Tyr Gly Gly Ser Ser
85 90 95

Tyr Ser Glu Arg Ala Glu Thr Val Val Glu Glu Val Lys Glu Met Phe
100 105 110

Asn Ser Ile Pro Asn Asn Arg Glu Leu Phe Gly Ser Gln Asn Asp Leu
115 120 125

Leu Thr Arg Leu Trp Met Val Asp Ser Ile Glu Arg Leu Gly Ile Asp
130 135 140

Arg His Phe Gln Asn Glu Ile Arg Val Ala Leu Asp Tyr Val Tyr Ser
145 150 155 160

Tyr Trp Lys Glu Lys Glu Gly Ile Gly Cys Gly Arg Asp Ser Thr Phe
165 170 175

Pro Asp Leu Asn Ser Thr Ala Leu Ala Leu Arg Thr Leu Arg Leu His
180 185 190

Gly Tyr Asn Val Ser Ser Asp Val Leu Glu Tyr Phe Lys Asp Glu Lys
195 200 205

Gly His Phe Ala Cys Pro Ala Ile Leu Thr Glu Gly Gln Ile Thr Arg
210 215 220

Ser Val Leu Asn Leu Tyr Arg Ala Ser Leu Val Ala Phe Pro Gly Glu
225 230 235 240

Lys Val Met Glu Glu Ala Glu Ile Phe Ser Ala Ser Tyr Leu Lys Lys
245 250 255

Val Leu Gln Lys Ile Pro Val Ser Asn Leu Ser Gly Glu Ile Glu Tyr
260 265 270

Val Leu Glu Tyr Gly Trp His Thr Asn Leu Pro Arg Leu Glu Ala Arg
275 280 285

Asn Tyr Ile Glu Val Tyr Glu Gln Ser Gly Tyr Glu Ser Leu Asn Glu
290 295 300

Met Pro Tyr Met Asn Met Lys Lys Leu Leu Gln Leu Ala Lys Leu Glu
305 310 315 320

Phe Asn Ile Phe His Ser Leu Gln Leu Arg Glu Leu Gln Ser Ile Ser
325 330 335

Arg Trp Trp Lys Glu Ser Gly Ser Ser Gln Leu Thr Phe Thr Arg His
340 345 350

Arg His Val Glu Tyr Tyr Thr Met Ala Ser Cys Ile Ser Met Leu Pro
355 360 365

Lys His Ser Ala Phe Arg Met Glu Phe Val Lys Val Cys His Leu Val
370 375 380

Thr Val Leu Asp Asp Ile Tyr Asp Thr Phe Gly Thr Met Asn Glu Leu
385 390 395 400

Gln Leu Phe Thr Asp Ala Ile Lys Arg Trp Asp Leu Ser Thr Thr Arg
405 410 415

Trp Leu Pro Glu Tyr Met Lys Gly Val Tyr Met Asp Leu Tyr Gln Cys
420 425 430

Ile Asn Glu Met Val Glu Glu Ala Glu Lys Thr Gln Gly Arg Asp Met
435 440 445

Leu Asn Tyr Ile Gln Asn Ala Trp Glu Ala Leu Phe Asp Thr Phe Met
450 455 460

Gln Glu Ala Lys Trp Ile Ser Ser Ser Tyr Leu Pro Thr Phe Glu Glu
465 470 475 480

Tyr Leu Lys Asn Ala Lys Val Ser Ser Gly Ser Arg Ile Ala Thr Leu

485

490

495

Gln Pro Ile Leu Thr Leu Asp Val Pro Leu Pro Asp Tyr Ile Leu Gln
500 505 510

Glu Ile Asp Tyr Pro Ser Arg Phe Asn Glu Leu Ala Ser Ser Ile Leu
515 520 525

Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys Ala Asp Arg Ala Arg Gly
530 535 540

Glu Glu Ala Ser Ala Ile Ser Cys Tyr Met Lys Asp His Pro Gly Ser
545 550 555 560

Ile Glu Glu Asp Ala Leu Asn His Ile Asn Ala Met Ile Ser Asp Ala
565 570 575

Ile Arg Glu Leu Asn Trp Glu Leu Leu Arg Pro Asp Ser Lys Ser Pro
580 585 590

Ile Ser Ser Lys Lys His Ala Phe Asp Ile Thr Arg Ala Phe His His
595 600 605

Val Tyr Lys Tyr Arg Asp Gly Tyr Thr Val Ser Asn Asn Glu Thr Lys
610 615 620

Asn Leu Val Met Lys Thr Val Leu Glu Pro Leu Ala Leu
625 630 635

<210> 7
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Degenerate
oligonucleotide PCR primer A wherein the letter
"n" indicates an inosine residue

<220>
<221> misc_feature
<222> (1)..(25)
<223> Degenerate oligonucleotide Primer A wherein n
represents inosine

<400> 7
arraygarra nggnrartay aarga

25

<210> 8
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: degenerate
oligonucleotide PCR primer B wherein the letter
"n" represents an inosine residue

<220>

<221> misc_feature
<222> (1)..(20)
<223> oligonucleotide PCR primer B wherein the letter n
represents an inosine residue

<400> 8
atgytnrary tntaygargc

20

<210> 9
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: degenerate
oligonucleotide PCR primer C wherein the letter
"n" represents an inosine residue

<220>
<221> misc_feature
<222> (1)..(24)
<223> PCR primer C wherein the letter n represents
inosine

<400> 9
ctnkynrang gnctratrta ckty

24

<210> 10
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: degenerate
oligonucleotide PCR primer D wherein the letter
"n" represents an inosine residue

<220>
<221> misc_feature
<222> (1)..(23)
<223> PCR primer D wherein the letter n represents
inosine

<400> 10
gaygaynnnt wygaygcnya ygg

23

<210> 11
<211> 108
<212> DNA
<213> Artificial Sequence

<400> 11
gatgatgggt ttgatgcgca cggAACCTA gatgaattga agtattcac tgaggctgtg 60
agaagatggg acctctccctt tacagacaac ttccccgatt acatgaaa

108

<210> 12

<211> 104

<212> DNA

<213> Abies grandis

<400> 12

gacgacgggt atgatgcgca tggaacgatt gacgagcttg aactcttcac atctgcaatt 60

aagagatgga attcatcaga gatagacagc ttccccgact atat

104

<210> 13

<211> 105

<212> DNA

<213> Abies grandis

<220>

<221> misc_feature

<222> (89)

<223> nucleotide may be a or c or g or t

<400> 13

gatgatgggt atgatgcgta cggaacgttg gaagaaatca aaatcatgac agagggagtg 60

agacgatggg atcttcgtt gaccgcttnc cccgactata tgaaa

105

<210> 14

<211> 117

<212> DNA

<213> Abies grandis

<220>

<221> misc_feature

<222> (93)

<223> nucleotide may be a or c or g or t

<400> 14

gacgatgggt atgatgcgca tggaaccttg gaccaactca aaatctttac agagggagtg 60

agacgatggg atgttcgtt ggttagaccac ttncccccac tacatgaat cttagacc 117

<210> 15

<211> 2424

<212> DNA

<213> Abies grandis

<220>

<221> CDS

<222> (2)..(2350)

<223> Clone AG1.28

<400> 15

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Gly Tyr Asp Leu Val His Ser Leu Lys Ser Pro Tyr Ile Asp Ser Ser

1 5 10 15

tac aga gaa cgc gcg gag gtc ctt gtt agc gag att aaa gtg atg ctt 97

Tyr Arg Glu Arg Ala Glu Val Leu Val Ser Glu Ile Lys Val Met Leu

20 25 30

aat cca gct att aca gga gat gga gaa tca atg att act cca tct gct 145
Asn Pro Ala Ile Thr Gly Asp Gly Glu Ser Met Ile Thr Pro Ser Ala
35 40 45

tat gac aca gca tgg gta gcg agg gtg ccc gcc att gat ggc tct gct 193
Tyr Asp Thr Ala Trp Val Ala Arg Val Pro Ala Ile Asp Gly Ser Ala
50 55 60

cgc ccg caa ttt ccc caa aca gtt gac tgg att ttg aaa aac cag tta 241
Arg Pro Gln Phe Pro Gln Thr Val Asp Trp Ile Leu Lys Asn Gln Leu
65 70 75 80

aaa gat ggt tca tgg gga att cag tcc cac ttt ctg ctg tcc gac cgt 289
Lys Asp Gly Ser Trp Gly Ile Gln Ser His Phe Leu Leu Ser Asp Arg
85 90 95

ctt ctt gcc act ctt tct tgt gtt ctt gtg ctc ctt aaa tgg aac gtt 337
Leu Leu Ala Thr Leu Ser Cys Val Leu Val Leu Leu Lys Trp Asn Val
100 105 110

ggg gat ctg caa gta gag cag gga att gaa ttc ata aag agc aat ctg 385
Gly Asp Leu Gln Val Glu Gln Gly Ile Glu Phe Ile Lys Ser Asn Leu
115 120 125

gaa cta gta aag gat gaa acc gat caa gat agc ttg gta aca gac ttt 433
Glu Leu Val Lys Asp Glu Thr Asp Gln Asp Ser Leu Val Thr Asp Phe
130 135 140

gag atc ata ttt cct tct ctg tta aga gaa gct caa tct ctg cgc ctc 481
Glu Ile Ile Phe Pro Ser Leu Leu Arg Glu Ala Gln Ser Leu Arg Leu
145 150 155 160

gga ctt ccc tac gac ctg cct tat ata cat ctg ttg cag act aaa cgg 529
Gly Leu Pro Tyr Asp Leu Pro Tyr Ile His Leu Leu Gln Thr Lys Arg
165 170 175

cag gaa aga tta gca aaa ctt tca agg gag gaa att tat gcg gtt ccg 577
Gln Glu Arg Leu Ala Lys Leu Ser Arg Glu Glu Ile Tyr Ala Val Pro
180 185 190

tcg cca ttg ttg tat tct tta gag gga ata caa gat ata gtt gaa tgg 625
Ser Pro Leu Leu Tyr Ser Leu Glu Gly Ile Gln Asp Ile Val Glu Trp
195 200 205

gaa cga ata atg gaa gtt caa agt cag gat ggg tct ttc tta agc tca 673
Glu Arg Ile Met Glu Val Gln Ser Gln Asp Gly Ser Phe Leu Ser Ser
210 215 220

cct gct tct act gcc tgc gtt ttc atg cac aca gga gac gcg aaa tgc 721
Pro Ala Ser Thr Ala Cys Val Phe Met His Thr Gly Asp Ala Lys Cys
225 230 235 240

ctt gaa ttc ttg aac agt gtg atg atc aag ttt gga aat ttt gtt ccc 769
Leu Glu Phe Leu Asn Ser Val Met Ile Lys Phe Gly Asn Phe Val Pro
245 250 255

tgc ctg tat cct gtg gat ctg ctg gaa cgc ctg ttg atc gta gat aat 817
Cys Leu Tyr Pro Val Asp Leu Leu Glu Arg Leu Leu Ile Val Asp Asn
260 265 270

att gta cgc ctt gga atc tat aga cac ttt gaa aag gaa atc aag gaa 865

Ile Val Arg Leu Gly Ile Tyr Arg His Phe Glu Lys Glu Ile Lys Glu
275 280 285

gct ctt gat tat gtt tac agg cat tgg aac gaa aga gga att ggg tgg 913
Ala Leu Asp Tyr Val Tyr Arg His Trp Asn Glu Arg Gly Ile Gly Trp
290 295 300

ggc aga cta aat ccc ata gca gat ctt gag acc act gct ttg gga ttt 961
Gly Arg Leu Asn Pro Ile Ala Asp Leu Glu Thr Thr Ala Leu Gly Phe
305 310 315 320

cga ttg ctt cgg ctg cat agg tac aat gta tct cca gcc att ttt gac 1009
Arg Leu Leu Arg Leu His Arg Tyr Asn Val Ser Pro Ala Ile Phe Asp
325 330 335

aac ttc aaa gat gcc aat ggg aaa ttc att tgc tcg acc ggt caa ttc 1057
Asn Phe Lys Asp Ala Asn Gly Lys Phe Ile Cys Ser Thr Gly Gln Phe
340 345 350

aac aaa gat gta gca agc atg ctg aat ctt tat aga gct tcc cag ctc 1105
Asn Lys Asp Val Ala Ser Met Leu Asn Leu Tyr Arg Ala Ser Gln Leu
355 360 365

gca ttt ccc gga gaa aac att ctt gat gaa gct aaa agc ttc gct act 1153
Ala Phe Pro Gly Glu Asn Ile Leu Asp Glu Ala Lys Ser Phe Ala Thr
370 375 380

aaa tat ttg aga gaa gct ctt gag aaa agt gag act tcc agt gca tgg 1201
Lys Tyr Leu Arg Glu Ala Leu Glu Lys Ser Glu Thr Ser Ser Ala Trp
385 390 395 400

aac aac aaa caa aac ctg agc caa gag atc aaa tac gcg ctg aag act 1249
Asn Asn Lys Asn Leu Ser Gln Glu Ile Lys Tyr Ala Leu Lys Thr
405 410 415

tct tgg cat gcc agt gtt ccg aga gtg gaa gca aag aga tac tgt caa 1297
Ser Trp His Ala Ser Val Pro Arg Val Glu Ala Lys Arg Tyr Cys Gln
420 425 430

gtg tat cgc cca gat tat gca cgc ata gca aaa tgc gtt tac aag cta 1345
Val Tyr Arg Pro Asp Tyr Ala Arg Ile Ala Lys Cys Val Tyr Lys Leu
435 440 445

ccc tac gtg aac aat gaa aag ttt tta gag ctg gga aaa tta gat ttc 1393
Pro Tyr Val Asn Asn Glu Lys Phe Leu Glu Ieu Gly Lys Leu Asp Phe
450 455 460

aac att atc cag tcc atc cac caa gaa gaa atg aag aat gtt acc agc 1441
Asn Ile Ile Gln Ser Ile His Gln Glu Glu Met Lys Asn Val Thr Ser
465 470 475 480

tgg ttt aga gat tcg ggg ttg cca cta ttc acc ttc gct cgg gag agg 1489
Trp Phe Arg Asp Ser Gly Leu Pro Leu Phe Thr Phe Ala Arg Glu Arg
485 490 495

ccg ctg gaa ttc tac ttc tta gta gcg gcg ggg acc tat gaa ccc cag 1537
Pro Leu Glu Phe Tyr Phe Leu Val Ala Ala Gly Thr Tyr Glu Pro Gln
500 505 510

tat gcc aaa tgc agg ttc ctc ttt aca aaa gtg gca tgc ttg cag act 1585
Tyr Ala Lys Cys Arg Phe Leu Phe Thr Lys Val Ala Cys Leu Gln Thr

515

520

525

gtt ctg gac gat atg tat gac act tat gga acc cta gat gaa ttg aag Val Leu Asp Asp Met Tyr Asp Thr Tyr Gly Thr Leu Asp Glu Leu Lys 530 535 540	1633
cta ttc act gag gct gtg aga aga tgg gac ctc tcc ttt aca gaa aac Leu Phe Thr Glu Ala Val Arg Arg Trp Asp Leu Ser Phe Thr Glu Asn 545 550 555 560	1681
ctt cca gac tat atg aaa cta tgt tac caa atc tat tat gac ata gtt Leu Pro Asp Tyr Met Lys Leu Cys Tyr Gln Ile Tyr Tyr Asp Ile Val 565 570 575	1729
cac gag gtg gct tgg gag gca gag aag gaa cag ggg cgt gaa ttg gtc His Glu Val Ala Trp Glu Ala Glu Lys Glu Gln Gly Arg Glu Leu Val 580 585 590	1777
agc ttt ttc aga aag gga tgg gag gat tat ctt ctg ggt tat tat gaa Ser Phe Phe Arg Lys Gly Trp Glu Asp Tyr Leu Leu Gly Tyr Tyr Glu 595 600 605	1825
gaa gct gaa tgg tta gct gct gag tat gtg cct acc ttg gac gag tac Glu Ala Glu Trp Leu Ala Ala Glu Tyr Val Pro Thr Leu Asp Glu Tyr 610 615 620	1873
ata aag aat gga atc aca tct atc ggc caa cgt ata ctt ctg ttg agt Ile Lys Asn Gly Ile Thr Ser Ile Gly Gln Arg Ile Leu Leu Leu Ser 625 630 635 640	1921
gga gtg ttg ata atg gat ggg caa ctc ctt tcg caa gag gca tta gag Gly Val Leu Ile Met Asp Gly Gln Leu Leu Ser Gln Glu Ala Leu Glu 645 650 655	1969
aaa gta gat tat cca gga aga cgt gtt ctc aca gag ctg aat agc ctc Lys Val Asp Tyr Pro Gly Arg Arg Val Leu Thr Glu Leu Asn Ser Leu 660 665 670	2017
att tcc cgc ctg gcg gat gac acg aag aca tat aaa gct gag aag gct Ile Ser Arg Leu Ala Asp Asp Thr Lys Thr Tyr Lys Ala Glu Lys Ala 675 680 685	2065
cgt gga gaa ttg gcg tcc agc att gaa tgt tac atg aaa gac cat cct Arg Gly Glu Leu Ala Ser Ser Ile Glu Cys Tyr Met Lys Asp His Pro 690 695 700	2113
gaa tgt aca gag gaa gag gct ctc gat cac atc tat agc att ctg gag Glu Cys Thr Glu Glu Ala Leu Asp His Ile Tyr Ser Ile Leu Glu 705 710 715 720	2161
ccg gcg gtg aag gaa ctg aca aga gag ttt ctg aag ccc gac gac gtc Pro Ala Val Lys Glu Leu Thr Arg Glu Phe Leu Lys Pro Asp Asp Val 725 730 735	2209
cca ttc gcc tgc aag aag atg ctt ttc gag gag aca aga gtg acg atg Pro Phe Ala Cys Lys Lys Met Leu Phe Glu Glu Thr Arg Val Thr Met 740 745 750	2257
gtg ata ttc aag gat gga gat gga ttc ggt gtt tcc aaa tta gaa gtc Val Ile Phe Lys Asp Gly Asp Gly Phe Gly Val Ser Lys Leu Glu Val 755 760 765	2305

HUMAN CHOROID NEVUS PROTEIN

aaa gat cat atc aaa gag tgt ctc att gaa ccg ctg cca ctg taa 2350
Lys Asp His Ile Lys Glu Cys Leu Ile Glu Pro Leu Pro Leu
770 775 780

tcaaaaatagt tgcaataata attgaaataa tgtcaactat gtttcacaaa aaaaaaaaaa 2410
aaaaaaaaaaaa aaaa 2424

<210> 16
<211> 782
<212> PRT
<213> Abies grandis

<400> 16
Gly Tyr Asp Leu Val His Ser Leu Lys Ser Pro Tyr Ile Asp Ser Ser
1 5 10 15

Tyr Arg Glu Arg Ala Glu Val Leu Val Ser Glu Ile Lys Val Met Leu
20 25 30

Asn Pro Ala Ile Thr Gly Asp Gly Glu Ser Met Ile Thr Pro Ser Ala
35 40 45

Tyr Asp Thr Ala Trp Val Ala Arg Val Pro Ala Ile Asp Gly Ser Ala
50 55 60

Arg Pro Gln Phe Pro Gln Thr Val Asp Trp Ile Leu Lys Asn Gln Leu
65 70 75 80

Lys Asp Gly Ser Trp Gly Ile Gln Ser His Phe Leu Leu Ser Asp Arg
85 90 95

Leu Leu Ala Thr Leu Ser Cys Val Leu Val Leu Lys Trp Asn Val
100 105 110

Gly Asp Leu Gln Val Glu Gln Gly Ile Glu Phe Ile Lys Ser Asn Leu
115 120 125

Glu Leu Val Lys Asp Glu Thr Asp Gln Asp Ser Leu Val Thr Asp Phe
130 135 140

Glu Ile Ile Phe Pro Ser Leu Leu Arg Glu Ala Gln Ser Leu Arg Leu
145 150 155 160

Gly Leu Pro Tyr Asp Leu Pro Tyr Ile His Leu Leu Gln Thr Lys Arg
165 170 175

Gln Glu Arg Leu Ala Lys Leu Ser Arg Glu Glu Ile Tyr Ala Val Pro
180 185 190

Ser Pro Leu Leu Tyr Ser Leu Glu Gly Ile Gln Asp Ile Val Glu Trp
195 200 205

Glu Arg Ile Met Glu Val Gln Ser Gln Asp Gly Ser Phe Leu Ser Ser
210 215 220

Pro Ala Ser Thr Ala Cys Val Phe Met His Thr Gly Asp Ala Lys Cys
225 230 235 240

Leu Glu Phe Leu Asn Ser Val Met Ile Lys Phe Gly Asn Phe Val Pro
245 250 255

Cys Leu Tyr Pro Val Asp Leu Leu Glu Arg Leu Leu Ile Val Asp Asn
260 265 270

Ile Val Arg Leu Gly Ile Tyr Arg His Phe Glu Lys Glu Ile Lys Glu
275 280 285

Ala Leu Asp Tyr Val Tyr Arg His Trp Asn Glu Arg Gly Ile Gly Trp
290 295 300

Gly Arg Leu Asn Pro Ile Ala Asp Leu Glu Thr Thr Ala Leu Gly Phe
305 310 315 320

Arg Leu Leu Arg Leu His Arg Tyr Asn Val Ser Pro Ala Ile Phe Asp
325 330 335

Asn Phe Lys Asp Ala Asn Gly Lys Phe Ile Cys Ser Thr Gly Gln Phe
340 345 350

Asn Lys Asp Val Ala Ser Met Leu Asn Leu Tyr Arg Ala Ser Gln Leu
355 360 365

Ala Phe Pro Gly Glu Asn Ile Leu Asp Glu Ala Lys Ser Phe Ala Thr
370 375 380

Lys Tyr Leu Arg Glu Ala Leu Glu Lys Ser Glu Thr Ser Ser Ala Trp
385 390 395 400

Asn Asn Lys Gln Asn Leu Ser Gln Glu Ile Lys Tyr Ala Leu Lys Thr
405 410 415

Ser Trp His Ala Ser Val Pro Arg Val Glu Ala Lys Arg Tyr Cys Gln
420 425 430

Val Tyr Arg Pro Asp Tyr Ala Arg Ile Ala Lys Cys Val Tyr Lys Leu
435 440 445

Pro Tyr Val Asn Asn Glu Lys Phe Leu Glu Leu Gly Lys Leu Asp Phe
450 455 460

Asn Ile Ile Gln Ser Ile His Gln Glu Glu Met Lys Asn Val Thr Ser
465 470 475 480

Trp Phe Arg Asp Ser Gly Leu Pro Leu Phe Thr Phe Ala Arg Glu Arg
485 490 495

Pro Leu Glu Phe Tyr Phe Leu Val Ala Ala Gly Thr Tyr Glu Pro Gln
500 505 510

Tyr Ala Lys Cys Arg Phe Leu Phe Thr Lys Val Ala Cys Leu Gln Thr
515 520 525

Val Leu Asp Asp Met Tyr Asp Thr Tyr Gly Thr Leu Asp Glu Leu Lys
530 535 540

Leu Phe Thr Glu Ala Val Arg Arg Trp Asp Leu Ser Phe Thr Glu Asn
545 550 555 560

Leu Pro Asp Tyr Met Lys Leu Cys Tyr Gln Ile Tyr Tyr Asp Ile Val

565

570

575

His Glu Val Ala Trp Glu Ala Glu Lys Glu Gln Gly Arg Glu Leu Val
580 585 590

Ser Phe Phe Arg Lys Gly Trp Glu Asp Tyr Leu Leu Gly Tyr Tyr Glu
595 600 605

Glu Ala Glu Trp Leu Ala Ala Glu Tyr Val Pro Thr Leu Asp Glu Tyr
610 615 620

Ile Lys Asn Gly Ile Thr Ser Ile Gly Gln Arg Ile Leu Leu Leu Ser
625 630 635 640

Gly Val Leu Ile Met Asp Gly Gln Leu Leu Ser Gln Glu Ala Leu Glu
645 650 655

Lys Val Asp Tyr Pro Gly Arg Arg Val Leu Thr Glu Leu Asn Ser Leu
660 665 670

Ile Ser Arg Leu Ala Asp Asp Thr Lys Thr Tyr Lys Ala Glu Lys Ala
675 680 685

Arg Gly Glu Leu Ala Ser Ser Ile Glu Cys Tyr Met Lys Asp His Pro
690 695 700

Glu Cys Thr Glu Glu Ala Leu Asp His Ile Tyr Ser Ile Leu Glu
705 710 715 720

Pro Ala Val Lys Glu Leu Thr Arg Glu Phe Leu Lys Pro Asp Asp Val
725 730 735

Pro Phe Ala Cys Lys Lys Met Leu Phe Glu Glu Thr Arg Val Thr Met
740 745 750

Val Ile Phe Lys Asp Gly Asp Gly Phe Gly Val Ser Lys Leu Glu Val
755 760 765

Lys Asp His Ile Lys Glu Cys Leu Ile Glu Pro Leu Pro Leu
770 775 780

<210> 17

<211> 1967

<212> DNA

<213> Abies grandis

<220>

<221> CDS

<222> (3)...(1736)

<223> Clone AG4.30

<400> 17

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Ser Glu Ser Ser Ile Pro Arg Arg Thr Gly Asn His His Gly Asn
1 5 10 15

47

gtg tgg gac gat gac ctc ata cac tct ctc aac tcg ccc tat ggg gca
Val Trp Asp Asp Asp Leu Ile His Ser Leu Asn Ser Pro Tyr Gly Ala
20 25 30

95

cct gca tat tat gag ctc ctt caa aag ctt att gag gag atc aag cat
Pro Ala Tyr Tyr Glu Leu Leu Gln Lys Leu Ile Glu Glu Ile Lys His 143
35 40 45

tta ctt ttg act gaa atg gaa atg gat gat ggc gat cat gat tta atc
Leu Leu Leu Thr Glu Met Glu Met Asp Asp Gly Asp His Asp Leu Ile 191
50 55 60

aaa cgt ctt cag atc gtt gac act ttg gaa tgc ctg gga atc gat aga
Lys Arg Leu Gln Ile Val Asp Thr Leu Glu Cys Leu Gly Ile Asp Arg 239
65 70 75

cat ttt gaa cac gaa ata caa aca gct gct tta gat tac gtt tac aga
His Phe Glu His Glu Ile Gln Thr Ala Ala Leu Asp Tyr Val Tyr Arg 287
80 85 90 95

tgg tgg aac gaa aaa ggt atc ggg gag gga tca aga gat tcc ttc agc
Trp Trp Asn Glu Lys Gly Ile Gly Glu Gly Ser Arg Asp Ser Phe Ser 335
100 105 110

aaa gat ctc aac gct aca gct tta gga ttt cgc gct ctc cga ctg cat
Lys Asp Leu Asn Ala Thr Ala Leu Gly Phe Arg Ala Leu Arg Leu His 383
115 120 125

cga tat aac gta tcg tca ggt gtg ttg aag aat ttc aag gat gaa aac
Arg Tyr Asn Val Ser Ser Gly Val Leu Lys Asn Phe Lys Asp Glu Asn 431
130 135 140

ggg aag ttc ttc tgc aac ttt act ggt gaa gaa gga aga gga gat aaa
Gly Lys Phe Phe Cys Asn Phe Thr Gly Glu Glu Gly Arg Gly Asp Lys 479
145 150 155

caa gtg aga agc atg ttg tcg tta ctt cga gct tca gag att tcg ttt
Gln Val Arg Ser Met Leu Ser Leu Leu Arg Ala Ser Glu Ile Ser Phe 527
160 165 170 175

ccc gga gaa aaa gtg atg gaa gag gcc aag gca ttc aca aga gaa tat
Pro Gly Glu Lys Val Met Glu Glu Ala Lys Ala Phe Thr Arg Glu Tyr 575
180 185 190

cta aac caa gtt tta gct gga cac ggg gat gtg act gac gtg gat caa
Leu Asn Gln Val Leu Ala Gly His Gly Asp Val Thr Asp Val Asp Gln 623
195 200 205

agc ctt ttg gag aga ggt gaa gta cgc att gga gtt tcc atg gct tgc
Ser Leu Leu Glu Arg Gly Glu Val Arg Ile Gly Val Ser Met Ala Cys 671
210 215 220

agt gtg ccg aga tgg gag gca agg agc ttt ctc gaa ata tat gga cac
Ser Val Pro Arg Trp Glu Ala Arg Ser Phe Leu Glu Ile Tyr Gly His 719
225 230 235

aac cat tcg tgg ctc aag tcg aat atc aac caa aaa atg ttg aag tta
Asn His Ser Trp Leu Lys Ser Asn Ile Asn Gln Lys Met Leu Lys Leu 767
240 245 250 255

gcc aaa ttg gac ttc aat att ctg caa tgc aaa cat cac aag gag ata
Ala Lys Leu Asp Phe Asn Ile Leu Gln Cys Lys His His Lys Glu Ile 815
260 265 270

cag ttt att aca agg tgg tgg aga gac tcg ggt ata tcg cag ctg aat 863

cct gca tat tat gag ctc ctt caa aag ctt att gag gag atc aag cat		143
Pro Ala Tyr Tyr Glu Leu Leu Gln Lys Leu Ile Glu Glu Ile Lys His		
35	40	45
tta ctt ttg act gaa atg gaa atg gat gat ggc gat cat gat tta atc		191
Leu Leu Leu Thr Glu Met Glu Met Asp Asp Gly Asp His Asp Leu Ile		
50	55	60
aaa cgt ctt cag atc gtt gac act ttg gaa tgc ctg gga atc gat aga		239
Lys Arg Leu Gln Ile Val Asp Thr Leu Glu Cys Leu Gly Ile Asp Arg		
65	70	75
cat ttt gaa cac gaa ata caa aca gct gct tta gat tac gtt tac aga		287
His Phe Glu His Glu Ile Gln Thr Ala Ala Leu Asp Tyr Val Tyr Arg		
80	85	90
95		
tgg tgg aac gaa aaa ggt atc ggg gag gga tca aga gat tcc ttc agc		335
Trp Trp Asn Glu Lys Gly Ile Gly Glu Gly Ser Arg Asp Ser Phe Ser		
100	105	110
aaa gat ctc aac gct aca gct tta gga ttt cgc gct ctc cga ctg cat		383
Lys Asp Leu Asn Ala Thr Ala Leu Gly Phe Arg Ala Leu Arg Leu His		
115	120	125
cga tat aac gta tcg tca ggt gtg ttg aag aat ttc aag gat gaa aac		431
Arg Tyr Asn Val Ser Ser Gly Val Leu Lys Asn Phe Lys Asp Glu Asn		
130	135	140
ggg aag ttc ttc tgc aac ttt act ggt gaa gaa gga aga gga gat aaa		479
Gly Lys Phe Phe Cys Asn Phe Thr Gly Glu Glu Gly Arg Gly Asp Lys		
145	150	155
caa gtg aga agc atg ttg tcg tta ctt cga gct tca gag att tcg ttt		527
Gln Val Arg Ser Met Leu Ser Leu Leu Arg Ala Ser Glu Ile Ser Phe		
160	165	170
175		
ccc gga gaa aaa gtg atg gaa gag gcc aag gca ttc aca aga gaa tat		575
Pro Gly Glu Lys Val Met Glu Glu Ala Lys Ala Phe Thr Arg Glu Tyr		
180	185	190
cta aac caa gtt tta gct gga cac ggg gat gtg act gac gtg gat caa		623
Leu Asn Gln Val Ala Gly His Gly Asp Val Thr Asp Val Asp Gln		
195	200	205
agc ctt ttg gag aga ggt gaa gta cgc att gga gtt tcc atg gct tgc		671
Ser Leu Leu Glu Arg Gly Glu Val Arg Ile Gly Val Ser Met Ala Cys		
210	215	220
agt gtg ccg aga tgg gag gca agg agc ttt ctc gaa ata tat gga cac		719
Ser Val Pro Arg Trp Glu Ala Arg Ser Phe Leu Glu Ile Tyr Gly His		
225	230	235
aac cat tcg tgg ctc aag tcg aat atc aac caa aaa atg ttg aag tta		767
Asn His Ser Trp Leu Lys Ser Asn Ile Asn Gln Lys Met Leu Lys Leu		
240	245	250
255		
gcc aaa ttg gac ttc aat att ctg caa tgc aaa cat cac aag gag ata		815
Ala Lys Leu Asp Phe Asn Ile Leu Gln Cys Lys His His Lys Glu Ile		
260	265	270
cag ttt att aca agg tgg tgg aga gac tcg ggt ata tcg cag ctg aat		863

Gln Phe Ile Thr Arg Trp Trp Arg Asp Ser Gly Ile Ser Gln Leu Asn
275 280 285

ttc tat cga aag cga cac gtg gaa tat tat tct tgg gtt atg tgc 911
Phe Tyr Arg Lys Arg His Val Glu Tyr Tyr Ser Trp Val Val Met Cys
290 295 300

att ttt gag cca gag ttc tct gaa agt aga att gcc ttc gcc aaa act 959
Ile Phe Glu Pro Glu Phe Ser Glu Ser Arg Ile Ala Phe Ala Lys Thr
305 310 315

gct atc cta tgt act gtt cta gat gac ctc tat gat acg cac gca acg 1007
Ala Ile Leu Cys Thr Val Leu Asp Asp Leu Tyr Asp Thr His Ala Thr
320 325 330 335

ttg cat gaa atc aaa atc atg aca gag gga gtg aga cga tgg gat ctt 1055
Leu His Glu Ile Lys Ile Met Thr Glu Gly Val Arg Arg Trp Asp Leu
340 345 350

tcg ttg aca gat gac ctc cca gac tac att aaa att gca ttc cag ttc 1103
Ser Leu Thr Asp Asp Leu Pro Asp Tyr Ile Lys Ile Ala Phe Gln Phe
355 360 365

ttc ttc aat aca gtg aat gaa ttg ata gtt gaa atc gtg aaa cgg caa 1151
Phe Phe Asn Thr Val Asn Glu Leu Ile Val Glu Ile Val Lys Arg Gln
370 375 380

ggg cgg gat atg aca acc ata gtt aaa gat tgc tgg aag cga tac att 1199
Gly Arg Asp Met Thr Thr Ile Val Lys Asp Cys Trp Lys Arg Tyr Ile
385 390 395

gag tct tat ctg caa gaa gcg gaa tgg ata gca act gga cat att ccc 1247
Glu Ser Tyr Leu Gln Glu Ala Glu Trp Ile Ala Thr Gly His Ile Pro
400 405 410 415

act ttt aac gaa tac ata aag aac ggc atg gct agc tca ggg atg tgt 1295
Thr Phe Asn Glu Tyr Ile Lys Asn Gly Met Ala Ser Ser Gly Met Cys
420 425 430

att gta aat ttg aat cca ctt ctc ttg ttg ggt aaa ctt ctc ccc gac 1343
Ile Val Asn Leu Asn Pro Leu Leu Leu Gly Lys Leu Leu Pro Asp
435 440 445

aac att ctg gag caa ata cat tct cca tcc aag atc ctg gac ctc tta 1391
Asn Ile Leu Glu Gln Ile His Ser Pro Ser Lys Ile Leu Asp Leu Leu
450 455 460

gaa ttg acg ggc aga atc gcc gat gac tta aaa gat ttc gag gac gag 1439
Glu Leu Thr Gly Arg Ile Ala Asp Asp Leu Lys Asp Phe Glu Asp Glu
465 470 475

aag gaa cgc ggg gag atg gct tca tct tta cag tgt tat atg aaa gaa 1487
Lys Glu Arg Gly Glu Met Ala Ser Ser Leu Gln Cys Tyr Met Lys Glu
480 485 490 495

aat cct gaa tct aca gtg gaa aat gct tta aat cac ata aaa ggc atc 1535
Asn Pro Glu Ser Thr Val Glu Asn Ala Leu Asn His Ile Lys Gly Ile
500 505 510

ctt aat cgt tcc ctt gag gaa ttt aat tgg gag ttt atg aag cag gat 1583
Leu Asn Arg Ser Leu Glu Glu Phe Asn Trp Glu Phe Met Lys Gln Asp

515

520

525

agt gtc cca atg tgt tgc aag aaa ttc act ttc aat ata ggt cga gga 1631
Ser Val Pro Met Cys Cys Lys Lys Phe Thr Phe Asn Ile Gly Arg Gly
530 535 540

ctt caa ttc atc tac aaa tac aga gac ggc tta tac att tct gac aag 1679
Leu Gln Phe Ile Tyr Lys Tyr Arg Asp Gly Leu Tyr Ile Ser Asp Lys
545 550 555

gaa gta aag gac cag ata ttc aaa att cta gtc cac caa gtt cca atg 1727
Glu Val Lys Asp Gln Ile Phe Lys Ile Leu Val His Gln Val Pro Met
560 565 570 575

gag gaa tag tgatggtctt gggttagtt gtctattatg gtatattgca 1776
Glu Glu

ttgacattta tgcttaaagg tgtttcttaa acgttttaggg cgaccgtta aataagttgg 1836

caataattaa tatttagaga ctggtagaa gtgttaggg cataaaattt cctatggctt 1896

atggcaagct acaaatttggaa attgttgtgt ttataatatt tttattttat ttaaaaaaaaa 1956

aaaaaaaaaa a 1967

<210> 18

<211> 577

<212> PRT

<213> Abies grandis

<400> 18

Ser Glu Ser Ser Ile Pro Arg Arg Thr Gly Asn His His Gly Asn Val
1 5 10 15

Trp Asp Asp Asp Leu Ile His Ser Leu Asn Ser Pro Tyr Gly Ala Pro
20 25 30

Ala Tyr Tyr Glu Leu Leu Gln Lys Leu Ile Glu Glu Ile Lys His Leu
35 40 45

Leu Leu Thr Glu Met Glu Met Asp Asp Gly Asp His Asp Leu Ile Lys
50 55 60

Arg Leu Gln Ile Val Asp Thr Leu Glu Cys Leu Gly Ile Asp Arg His
65 70 75 80

Phe Glu His Glu Ile Gln Thr Ala Ala Leu Asp Tyr Val Tyr Arg Trp
85 90 95

Trp Asn Glu Lys Gly Ile Gly Glu Gly Ser Arg Asp Ser Phe Ser Lys
100 105 110

Asp Leu Asn Ala Thr Ala Leu Gly Phe Arg Ala Leu Arg Leu His Arg
115 120 125

Tyr Asn Val Ser Ser Gly Val Leu Lys Asn Phe Lys Asp Glu Asn Gly
130 135 140

Lys Phe Phe Cys Asn Phe Thr Gly Glu Glu Gly Arg Gly Asp Lys Gln
145 150 155 160

Val Arg Ser Met Leu Ser Leu Leu Arg Ala Ser Glu Ile Ser Phe Pro
165 170 175

Gly Glu Lys Val Met Glu Glu Ala Lys Ala Phe Thr Arg Glu Tyr Leu
180 185 190

Asn Gln Val Leu Ala Gly His Gly Asp Val Thr Asp Val Asp Gln Ser
195 200 205

Leu Leu Glu Arg Gly Glu Val Arg Ile Gly Val Ser Met Ala Cys Ser
210 215 220

Val Pro Arg Trp Glu Ala Arg Ser Phe Leu Glu Ile Tyr Gly His Asn
225 230 235 240

His Ser Trp Leu Lys Ser Asn Ile Asn Gln Lys Met Leu Lys Leu Ala
245 250 255

Lys Leu Asp Phe Asn Ile Leu Gln Cys Lys His His Lys Glu Ile Gln
260 265 270

Phe Ile Thr Arg Trp Trp Arg Asp Ser Gly Ile Ser Gln Leu Asn Phe
275 280 285

Tyr Arg Lys Arg His Val Glu Tyr Tyr Ser Trp Val Val Met Cys Ile
290 295 300

Phe Glu Pro Glu Phe Ser Glu Ser Arg Ile Ala Phe Ala Lys Thr Ala
305 310 315 320

Ile Leu Cys Thr Val Leu Asp Asp Leu Tyr Asp Thr His Ala Thr Leu
325 330 335

His Glu Ile Lys Ile Met Thr Glu Gly Val Arg Arg Trp Asp Leu Ser
340 345 350

Leu Thr Asp Asp Leu Pro Asp Tyr Ile Lys Ile Ala Phe Gln Phe Phe
355 360 365

Phe Asn Thr Val Asn Glu Leu Ile Val Glu Ile Val Lys Arg Gln Gly
370 375 380

Arg Asp Met Thr Thr Ile Val Lys Asp Cys Trp Lys Arg Tyr Ile Glu
385 390 395 400

Ser Tyr Leu Gln Glu Ala Glu Trp Ile Ala Thr Gly His Ile Pro Thr
405 410 415

Phe Asn Glu Tyr Ile Lys Asn Gly Met Ala Ser Ser Gly Met Cys Ile
420 425 430

Val Asn Leu Asn Pro Leu Leu Leu Gly Lys Leu Leu Pro Asp Asn
435 440 445

Ile Leu Glu Gln Ile His Ser Pro Ser Lys Ile Leu Asp Leu Leu Glu
450 455 460

Leu Thr Gly Arg Ile Ala Asp Asp Leu Lys Asp Phe Glu Asp Glu Lys
465 470 475 480

Glu Arg Gly Glu Met Ala Ser Ser Leu Gln Cys Tyr Met Lys Glu Asn
485 490 495

Pro Glu Ser Thr Val Glu Asn Ala Leu Asn His Ile Lys Gly Ile Leu
500 505 510

Asn Arg Ser Leu Glu Glu Phe Asn Trp Glu Phe Met Lys Gln Asp Ser
515 520 525

Val Pro Met Cys Cys Lys Lys Phe Thr Phe Asn Ile Gly Arg Gly Leu
530 535 540

Gln Phe Ile Tyr Lys Tyr Arg Asp Gly Leu Tyr Ile Ser Asp Lys Glu
545 550 555 560

Val Lys Asp Gln Ile Phe Lys Ile Leu Val His Gln Val Pro Met Glu
565 570 575

Glu

<210> 19

<211> 1416

<212> DNA

<213> Abies grandis

<220>

<221> CDS

<222> (3)..(1199)

<223> Clone AG5.9

<400> 19

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Lys Val Met Glu Glu Ala Lys Ala Phe Thr Thr Asn Tyr Leu Lys
1 5 10 15

aaa gtt tta gca gga cgg gag gct acc cac gtc gat gaa agc ctt ttg 95
Lys Val Leu Ala Gly Arg Glu Ala Thr His Val Asp Glu Ser Leu Leu
20 25 30

gga gag gtg aag tac gca ttg gag ttt cca tgg cat tgc agt gtg cag 143
Gly Glu Val Lys Tyr Ala Leu Glu Phe Pro Trp His Cys Ser Val Gln
35 40 45

aga tgg gag gca agg agc ttt atc gaa ata ttt gga caa att gat tca 191
Arg Trp Glu Ala Arg Ser Phe Ile Glu Ile Phe Gly Gln Ile Asp Ser
50 55 60

gag ctt aag tcg aat ttg agc aaa aaa atg tta gag ttg gcg aaa ttg 239
Glu Leu Lys Ser Asn Leu Ser Lys Lys Met Leu Glu Leu Ala Lys Leu
65 70 75

gac ttc aat att ctg caa tgc aca cat cag aaa gaa ctg cag att atc 287
Asp Phe Asn Ile Leu Gln Cys Thr His Gln Lys Glu Leu Gln Ile Ile
80 85 90 95

tca agg tgg ttc gca gac tca agt ata gca tcc ctg aat ttc tat cgg 335
Ser Arg Trp Phe Ala Asp Ser Ser Ile Ala Ser Leu Asn Phe Tyr Arg
100 105 110

aaa tgt tac gtc gaa ttt tac ttt tgg atg gct gca gcc atc tcc gag 383

Lys Cys Tyr Val Glu Phe Tyr Phe Trp Met Ala Ala Ala Ile Ser Glu
115 120 125

ccg gag ttt tct gga agc aga gtt gcc ttc aca aaa att gct ata ctg 431
Pro Glu Phe Ser Gly Ser Arg Val Ala Phe Thr Lys Ile Ala Ile Leu
130 135 140

atg aca atg cta gat gac ctg tac gat act cac gga acc ttg gac caa 479
Met Thr Met Leu Asp Asp Leu Tyr Asp Thr His Gly Thr Leu Asp Gln
145 150 155

ctc aaa atc ttt aca gag gga gtg aga cga tgg gat gtt tcg ttg gta 527
Leu Lys Ile Phe Thr Glu Gly Val Arg Arg Trp Asp Val Ser Leu Val
160 165 170 175

gag ggc ctc cca gac ttc atg aaa att gca ttc gag ttc tgg tta aag 575
Glu Gly Leu Pro Asp Phe Met Lys Ile Ala Phe Glu Phe Trp Leu Lys
180 185 190

aca tct aat gaa ttg att gct gaa gct gtt aaa gcg caa ggg caa gat 623
Thr Ser Asn Glu Leu Ile Ala Glu Ala Val Lys Ala Gln Gly Gln Asp
195 200 205

atg gcg gcc tac ata aga aaa aat gca tgg gag cga tac ctt gaa gct 671
Met Ala Ala Tyr Ile Arg Lys Asn Ala Trp Glu Arg Tyr Leu Glu Ala
210 215 220

tat ctg caa gat gcg gaa tgg ata gcc act gga cat gtc ccc acc ttt 719
Tyr Leu Gln Asp Ala Glu Trp Ile Ala Thr Gly His Val Pro Thr Phe
225 230 235

gat gag tac ttg aat aat ggc aca cca aac act ggg atg tgt gta ttg 767
Asp Glu Tyr Leu Asn Asn Gly Thr Pro Asn Thr Gly Met Cys Val Leu
240 245 250 255

aat ttg att ccg ctt ctg tta atg ggt gaa cat tta cca atc gac att 815
Asn Leu Ile Pro Leu Leu Met Gly Glu His Leu Pro Ile Asp Ile
260 265 270

ctg gag caa ata ttc ttg ccc tcc agg ttc cac cat ctc att gaa ttg 863
Leu Glu Gln Ile Phe Leu Pro Ser Arg Phe His His Leu Ile Glu Leu
275 280 285

gct tcc agg ctc gtc gat gac gcg aga gat ttc cag gcg gag aag gat 911
Ala Ser Arg Leu Val Asp Asp Ala Arg Asp Phe Gln Ala Glu Lys Asp
290 295 300

cat ggg gat tta tcg tgt att gag tgt tat tta aaa gat cat cct gag 959
His Gly Asp Leu Ser Cys Ile Glu Cys Tyr Leu Lys Asp His Pro Glu
305 310 315

tct aca gta gaa gat gct tta aat cat gtt aat ggc ctc ctt ggc aat 1007
Ser Thr Val Glu Asp Ala Leu Asn His Val Asn Gly Leu Leu Gly Asn
320 325 330 335

tgc ctt ctg gaa atg aat tgg aag ttc tta aag aag cag gac agt gtg 1055
Cys Leu Leu Glu Met Asn Trp Lys Phe Leu Lys Lys Gln Asp Ser Val
340 345 350

cca ctc tcg tgt aag aag tac agc ttc cat gta ttg gca cga agc atc 1103
Pro Leu Ser Cys Lys Lys Tyr Ser Phe His Val Leu Ala Arg Ser Ile

355

360

365

caa ttc atg tac aat caa ggc gat ggc ttc tcc att tcg aac aaa gtg 1151
Gln Phe Met Tyr Asn Gln Gly Asp Gly Phe Ser Ile Ser Asn Lys Val
370 375 380

atc aag gat caa gtg cag aaa gtt ctt att gtc ccc gtg cct att tga 1199
Ile Lys Asp Gln Val Gln Lys Val Leu Ile Val Pro Val Pro Ile
385 390 395

tagtagatac tagatagtag attagtagct attagtattt atttcataatc aatatttact 1259
aatgctgatg atggtaaag tccattcaga ccaatcttg gtttattgga cttaaataaa 1319
tgaattaatt agttgtttt aaaattgtac tattractgt tggaaataat gtttcatta 1379
ttgaaaataac tagcacaact attttagtgt ggttgat 1416

<210> 20
<211> 398
<212> PRT
<213> Abies grandis

<400> 20
Lys Val Met Glu Glu Ala Lys Ala Phe Thr Thr Asn Tyr Leu Lys Lys
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Val Leu Ala Gly Arg Glu Ala Thr His Val Asp Glu Ser Leu Leu Gly
20 25 30

Glu Val Lys Tyr Ala Leu Glu Phe Pro Trp His Cys Ser Val Gln Arg
35 40 45

Trp Glu Ala Arg Ser Phe Ile Glu Ile Phe Gly Gln Ile Asp Ser Glu
50 55 60

Leu Lys Ser Asn Leu Ser Lys Lys Met Leu Glu Leu Ala Lys Leu Asp
65 70 75 80

Phe Asn Ile Leu Gln Cys Thr His Gln Lys Glu Leu Gln Ile Ile Ser
85 90 95

Arg Trp Phe Ala Asp Ser Ser Ile Ala Ser Leu Asn Phe Tyr Arg Lys
100 105 110

Cys Tyr Val Glu Phe Tyr Phe Trp Met Ala Ala Ala Ile Ser Glu Pro
115 120 125

Glu Phe Ser Gly Ser Arg Val Ala Phe Thr Lys Ile Ala Ile Leu Met
130 135 140

Thr Met Leu Asp Asp Leu Tyr Asp Thr His Gly Thr Leu Asp Gln Leu
145 150 155 160

Lys Ile Phe Thr Glu Gly Val Arg Arg Trp Asp Val Ser Leu Val Glu
165 170 175

Gly Leu Pro Asp Phe Met Lys Ile Ala Phe Glu Phe Trp Leu Lys Thr
180 185 190

Ser Asn Glu Leu Ile Ala Glu Ala Val Lys Ala Gln Gly Gln Asp Met
195 200 205

Ala Ala Tyr Ile Arg Lys Asn Ala Trp Glu Arg Tyr Leu Glu Ala Tyr
210 215 220

Leu Gln Asp Ala Glu Trp Ile Ala Thr Gly His Val Pro Thr Phe Asp
225 230 235 240

Glu Tyr Leu Asn Asn Gly Thr Pro Asn Thr Gly Met Cys Val Leu Asn
245 250 255

Leu Ile Pro Leu Leu Leu Met Gly Glu His Leu Pro Ile Asp Ile Leu
260 265 270

Glu Gln Ile Phe Leu Pro Ser Arg Phe His His Leu Ile Glu Leu Ala
275 280 285

Ser Arg Leu Val Asp Asp Ala Arg Asp Phe Gln Ala Glu Lys Asp His
290 295 300

Gly Asp Leu Ser Cys Ile Glu Cys Tyr Leu Lys Asp His Pro Glu Ser
305 310 315 320

Thr Val Glu Asp Ala Leu Asn His Val Asn Gly Leu Leu Gly Asn Cys
325 330 335

Leu Leu Glu Met Asn Trp Lys Phe Leu Lys Lys Gln Asp Ser Val Pro
340 345 350

Leu Ser Cys Lys Lys Tyr Ser Phe His Val Leu Ala Arg Ser Ile Gln
355 360 365

Phe Met Tyr Asn Gln Gly Asp Gly Phe Ser Ile Ser Asn Lys Val Ile
370 375 380

Lys Asp Gln Val Gln Lys Val Leu Ile Val Pro Val Pro Ile
385 390 395

<210> 21

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide PCR primer E wherein the letter
"n" represents an inosine residue

<220>

<221> misc_feature

<222> (1)..(23)

<223> PCR primer E wherein the letter n represents
inosine

<400> 21

ggngaramrr tnatggarga rgc

23

<210> 22

<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: degenerate oligonucleotide primer F wherein the letter "n" represents an inosine residue

<220>
<221> misc_feature
<222> (1)..(24)
<223> PCR primer F wherein the letter n represents inosine

<400> 22
garytnccy tnhbnnmgnngt gttgg 24

<210> 23
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: degenerate oligonucleotide PCR primer G wherein the letter "n" represents an inosine residue

<220>
<221> misc_feature
<222> (1)..(21)
<223> PCR primer G wherein the letter n represents inosine

<400> 23
ccarttnarn ccytttnacrt c 21

<210> 24
<211> 533
<212> DNA
<213> Abies grandis

<400> 24
ggggaaaaaaa tgatggagga agctgaaatc ttctctacca aatatttaaa agaaggccctg 60
caaaaagattc cggtctccag tcttcgcga gagatcgaaa acgttttggaa atatggttgg 120
cacacatatt tgccgcgatt ggaaggcaagg aattacatcc aagtctttgg acaggacact 180
gagaacacgaa agtcatatgt gaagagcaaa aaacttttag aactcgcaaa attggagttc 240
aacatcttc aatccttact cgcataatccg cattgcaacc cattctgaca atggacatcc 300
cctttcctga tcataatcctc aaggaagttg acttcccattc aaagcttaac gacttggcat 360
gtgccatcct tcgattacga ggtgatacgc ggtgctacaa ggcggacagg gctcgtggag 420
aagaagcttc ctctatatca tgtttatatga aagacaatcc tggagttatca gaggaagatg 480

ctctcgatca tatcaacgcc atgatcagtg acgaagtcaa aggcttaat tgg 533

<210> 25
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: conserved amino acid motif on which the sequence of Primer D was based, wherein Xaa at position number 3 represents Thr or Ile, Xaa at position number 4 represents Ile or Tyr or Phe, Xaa at position number 6 represents Ala or Val and Xaa at position number 8 represents Ala or Gly

<220>
<221> SITE
<222> (1)..(8)
<223> conserved amino acid motif on which sequence of primer D was based

<400> 25
Asp Asp Xaa Xaa Asp Xaa Tyr Xaa
1 5

<210> 26
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: conserved amino acid motif on which the sequence of Primer E was based wherein Xaa at position 3 represents Lys or Thr, Xaa at position 4 represents Val or Ile, Xaa at position 6 represents Glu or Asp

<220>
<221> SITE
<222> (1)..(8)
<223> conserved amino acid sequence on which the sequence of primer E was based

<400> 26
Gly Glu Xaa Xaa Met Xaa Glu Ala
1 5

<210> 27
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: conserved amino acid sequence on which the sequence of primer F was based wherein Xaa at position 2 represents Phe or Tyr or Asp

Xaa at position 3 represents Ile or Leu, Xaa at position 4 represents Thr or
Leu
or Arg

<220>
<221> SITE
<222> (1)...(7)
<223> conserved amino acid sequence on which the
sequence of primer F was based

<400> 27
Gln Xaa Xaa Xaa Arg Trp Trp
1 5

<210> 28
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: conserved
amino acid motif on which the sequence of primer G
was based wherein Xaa at position 6 represents Phe or Leu

<220>
<221> SITE
<222> (1)...(8)
<223> conserved amino acid sequence on which the
sequence of primer G was based

<400> 28
Asp Val Ile Lys Gly Xaa Asn Trp
1 5

<210> 29
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: T3 primer
oligonucleotide sequence

<400> 29
aattaaccct cactaaaggg

20

<210> 30
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: T7
oligonucleotide primer sequence

<400> 30
gtaatacgcac tcactatagg gc

22

<210> 31
<211> 2205
<212> DNA
<213> Abies grandis

<220>
<221> CDS
<222> (57)..(1943)
<223> Clone AG3.48

<400> 31

gttatcttga gcttcctcca tataggccaa cacatatcat atcaaaggga gcaaga atg 59
Met
1

gct ctg gtt tct atc tca ccg ttg gct tcg aaa tct tgc ctg cgc aag 107
Ala Leu Val Ser Ile Ser Pro Leu Ala Ser Lys Ser Cys Leu Arg Lys
5 10 15

tcg ttg atc agt tca att cat gaa cat aag cct ccc tat aga aca atc 155
Ser Leu Ile Ser Ser Ile His Glu His Lys Pro Pro Tyr Arg Thr Ile
20 25 30

cca aat ctt gga atg cgt agg cga ggg aaa tct gtc acg cct tcc atg 203
Pro Asn Leu Gly Met Arg Arg Gly Lys Ser Val Thr Pro Ser Met
35 40 45

agc atc agt ttg gcc acc gct gca cct gat gat ggt gta caa aga cgc 251
Ser Ile Ser Leu Ala Ala Pro Asp Asp Gly Val Gln Arg Arg
50 55 60 65

ata ggt gac tac cat tcc aat atc tgg gac gat gat ttc ata cag tct 299
Ile Gly Asp Tyr His Ser Asn Ile Trp Asp Asp Asp Phe Ile Gln Ser
70 75 80

cta tca acg cat tat ggg gaa ccc tct tac cag gaa cgt gct gag aga 347
Leu Ser Thr His Tyr Gly Glu Pro Ser Tyr Gln Glu Arg Ala Glu Arg
85 90 95

tta att gtg gag gta aag aag ata ttc aat tca atg tac ctg gat gat 395
Leu Ile Val Glu Val Lys Lys Ile Phe Asn Ser Met Tyr Leu Asp Asp
100 105 110

gga aga tta atg agt tcc ttt aat gat ctc atg caa cgc ctt tgg ata 443
Gly Arg Leu Met Ser Ser Phe Asn Asp Leu Met Gln Arg Leu Trp Ile
115 120 125

gtc gat agc gtt gaa cgt ttg ggg ata gct aga cat ttc aag aac gag 491
Val Asp Ser Val Glu Arg Leu Gly Ile Ala Arg His Phe Lys Asn Glu
130 135 140 145

ata aca tca gct ctg gat tat gtt ttc cgt tac tgg gag gaa aac ggc 539
Ile Thr Ser Ala Leu Asp Tyr Val Phe Arg Tyr Trp Glu Glu Asn Gly
150 155 160

att gga tgt ggg aga gac agt att gtt act gat ctc aac tca act gcg 587
Ile Gly Cys Gly Arg Asp Ser Ile Val Thr Asp Leu Asn Ser Thr Ala
165 170 175

ttg ggg ttt cga act ctt cga tta cac ggg tac act gta tct cca gag 635

Leu Gly Phe Arg Thr Leu Arg Leu His Gly Tyr Thr Val Ser Pro Glu
180 185 190

gtt tta aaa gct ttt caa gat caa aat gga cag ttt gta tgc tcc ccc 683
Val Leu Lys Ala Phe Gln Asp Gln Asn Gly Gln Phe Val Cys Ser Pro
195 200 205

ggt cag aca gag ggt gag atc aga agc gtt ctt aac tta tat cgg gct 731
Gly Gln Thr Glu Gly Glu Ile Arg Ser Val Leu Asn Leu Tyr Arg Ala
210 215 220 225

tcc ctc att gcc ttc cct ggt gag aaa gtt atg gaa gaa gct gaa atc 779
Ser Leu Ile Ala Phe Pro Gly Glu Lys Val Met Glu Glu Ala Glu Ile
230 235 240

ttc tcc aca aga tat ttg aaa gaa gct cta caa aag att cca gtc tcc 827
Phe Ser Thr Arg Tyr Leu Lys Glu Ala Leu Gln Lys Ile Pro Val Ser
245 250 255

gct ctt tca caa gag ata aag ttt gtt atg gaa tat ggc tgg cac aca 875
Ala Leu Ser Gln Glu Ile Lys Phe Val Met Glu Tyr Gly Trp His Thr
260 265 270

aat ttg cca aga ttg gaa gca aga aat tac ata gac aca ctt gag aaa 923
Asn Leu Pro Arg Leu Glu Ala Arg Asn Tyr Ile Asp Thr Leu Glu Lys
275 280 285

gac acc agt gca tgg ctc aat aaa aat gct ggg aag aag ctt tta gaa 971
Asp Thr Ser Ala Trp Leu Asn Lys Asn Ala Gly Lys Lys Leu Leu Glu
290 295 300 305

ctt gca aaa ttg gag ttc aat ata ttt aac tcc tta caa caa aag gaa 1019
Leu Ala Lys Leu Glu Phe Asn Ile Phe Asn Ser Leu Gln Gln Lys Glu
310 315 320

tta caa tat ctt ttg aga tgg tgg aaa gag tcg gat ttg cct aaa ttg 1067
Leu Gln Tyr Leu Leu Arg Trp Trp Lys Glu Ser Asp Leu Pro Lys Leu
325 330 335

aca ttt gct cgg cat cgt cat gtg gaa ttc tac act ttg gcc tct tgt 1115
Thr Phe Ala Arg His Arg His Val Glu Phe Tyr Thr Leu Ala Ser Cys
340 345 350

att gcc att gac cca aaa cat tct gca ttc aga cta ggc ttc gcc aaa 1163
Ile Ala Ile Asp Pro Lys His Ser Ala Phe Arg Leu Gly Phe Ala Lys
355 360 365

atg tgt cat ctt gtc aca gtt ttg gac gat att tac gac act ttt gga 1211
Met Cys His Leu Val Thr Val Leu Asp Asp Ile Tyr Asp Thr Phe Gly
370 375 380 385

acg att gac gag ctt gaa ctc ttc aca tct gca att aag aga tgg aat 1259
Thr Ile Asp Glu Leu Glu Leu Phe Thr Ser Ala Ile Lys Arg Trp Asn
390 395 400

tca tca gag ata gaa cac ctt cca gaa tat atg aaa tgt gtg tac atg 1307
Ser Ser Glu Ile Glu His Leu Pro Glu Tyr Met Lys Cys Val Tyr Met
405 410 415

gtc gtg ttt gaa act gta aat gaa ctg aca cga gag gcg gag aag act 1355
Val Val Phe Glu Thr Val Asn Glu Leu Thr Arg Glu Ala Glu Lys Thr

420

425

430

caa ggg aga aac act ctc aac tat gtt cga aag gct tgg gag gct tat 1403
Gln Gly Arg Asn Thr Leu Asn Tyr Val Arg Lys Ala Trp Glu Ala Tyr
435 440 445

ttt gat tca tat atg gaa gaa gca aaa tgg atc tct aat ggt tat ctg 1451
Phe Asp Ser Tyr Met Glu Glu Ala Lys Trp Ile Ser Asn Gly Tyr Leu
450 455 460 465

cca acg ttt gaa gag tac cat gag aat ggg aaa gtg agc tct gca tat 1499
Pro Thr Phe Glu Glu Tyr His Glu Asn Gly Lys Val Ser Ser Ala Tyr
470 475 480

cgc gta gca aca ttg caa ccc atc ctc act ttg aat gca tgg ctt cct 1547
Arg Val Ala Thr Leu Gln Pro Ile Leu Thr Leu Asn Ala Trp Leu Pro
485 490 495

gat tac atc ttg aag gga att gat ttt cca tcc agg ttc aat gat ttg 1595
Asp Tyr Ile Leu Lys Gly Ile Asp Phe Pro Ser Arg Phe Asn Asp Leu
500 505 510

gca tcg tcc ttc ctt cgg cta cga ggt gac aca cgc tgc tac aag gcc 1643
Ala Ser Ser Phe Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys Ala
515 520 525

gat agg gat cgt ggt gaa gaa gct tcg tgt ata tca tgt tat atg aaa 1691
Asp Arg Asp Arg Gly Glu Glu Ala Ser Cys Ile Ser Cys Tyr Met Lys
530 535 540 545

gac aat cct gga tca acc gaa gaa gat gcc ctc aat cat atc aat gcc 1739
Asp Asn Pro Gly Ser Thr Glu Glu Asp Ala Leu Asn His Ile Asn Ala
550 555 560

atg gtc aat gac ata atc aaa gaa tta aat tgg gaa ctt cta aga tcc 1787
Met Val Asn Asp Ile Ile Lys Glu Leu Asn Trp Glu Leu Leu Arg Ser
565 570 575

aac gac aat att cca atg ctg gcc aag aaa cat gct ttt gac ata aca 1835
Asn Asp Asn Ile Pro Met Leu Ala Lys Lys His Ala Phe Asp Ile Thr
580 585 590

aga gct ctc cac cat ctc tac ata tat cga gat ggc ttt agt gtt gcc 1883
Arg Ala Leu His His Leu Tyr Ile Tyr Arg Asp Gly Phe Ser Val Ala
595 600 605

aac aag gaa aca aaa aaa ttg gtt atg gaa aca ctc ctt gaa tct atg 1931
Asn Lys Glu Thr Lys Lys Leu Val Met Glu Thr Leu Leu Glu Ser Met
610 615 620 625

ctt ttt taa cta taaccatatac cataataata agctcataat gctaaattat 1983
Leu Phe

tggccttatg acatagttt aatgtatgtact ttttgtgaatt caatcatatc gtgtgggtat 2043

gattaaaaag ctagagctta ctaggttagt aacatggtga taaaagttat aaaatgtgag 2103

ttatagagat acccatgttg aataatgaat tacaaaaaaga gaaattttagt tagaataaga 2163

tttggaaagctt ttcaattgtt ttaaaaaaaaaaaaaaaaaaa aa 2205

<210> 32
<211> 627
<212> PRT
<213> Abies grandis

<400> 32
Met Ala Leu Val Ser Ile Ser Pro Leu Ala Ser Lys Ser Cys Leu Arg
1 5 10 15
Lys Ser Leu Ile Ser Ser Ile His Glu His Lys Pro Pro Tyr Arg Thr
20 25 30
Ile Pro Asn Leu Gly Met Arg Arg Arg Gly Lys Ser Val Thr Pro Ser
35 40 45
Met Ser Ile Ser Leu Ala Thr Ala Ala Pro Asp Asp Gly Val Gln Arg
50 55 60
Arg Ile Gly Asp Tyr His Ser Asn Ile Trp Asp Asp Asp Phe Ile Gln
65 70 75 80
Ser Leu Ser Thr His Tyr Gly Glu Pro Ser Tyr Gln Glu Arg Ala Glu
85 90 95
Arg Leu Ile Val Glu Val Lys Lys Ile Phe Asn Ser Met Tyr Leu Asp
100 105 110
Asp Gly Arg Leu Met Ser Ser Phe Asn Asp Leu Met Gln Arg Leu Trp
115 120 125
Ile Val Asp Ser Val Glu Arg Leu Gly Ile Ala Arg His Phe Lys Asn
130 135 140
Glu Ile Thr Ser Ala Leu Asp Tyr Val Phe Arg Tyr Trp Glu Glu Asn
145 150 155 160
Gly Ile Gly Cys Gly Arg Asp Ser Ile Val Thr Asp Leu Asn Ser Thr
165 170 175
Ala Leu Gly Phe Arg Thr Leu Arg Leu His Gly Tyr Thr Val Ser Pro
180 185 190
Glu Val Leu Lys Ala Phe Gln Asp Gln Asn Gly Gln Phe Val Cys Ser
195 200 205
Pro Gly Gln Thr Glu Gly Glu Ile Arg Ser Val Leu Asn Leu Tyr Arg
210 215 220
Ala Ser Leu Ile Ala Phe Pro Gly Glu Lys Val Met Glu Glu Ala Glu
225 230 235 240
Ile Phe Ser Thr Arg Tyr Leu Lys Glu Ala Leu Gln Lys Ile Pro Val
245 250 255
Ser Ala Leu Ser Gln Glu Ile Lys Phe Val Met Glu Tyr Gly Trp His
260 265 270
Thr Asn Leu Pro Arg Leu Glu Ala Arg Asn Tyr Ile Asp Thr Leu Glu
275 280 285

Lys Asp Thr Ser Ala Trp Leu Asn Lys Asn Ala Gly Lys Lys Leu Leu
290 295 300

Glu Leu Ala Lys Leu Glu Phe Asn Ile Phe Asn Ser Leu Gln Gln Lys
305 310 315 320

Glu Leu Gln Tyr Leu Leu Arg Trp Trp Lys Glu Ser Asp Leu Pro Lys
325 330 335

Leu Thr Phe Ala Arg His Arg His Val Glu Phe Tyr Thr Leu Ala Ser
340 345 350

Cys Ile Ala Ile Asp Pro Lys His Ser Ala Phe Arg Leu Gly Phe Ala
355 360 365

Lys Met Cys His Leu Val Thr Val Leu Asp Asp Ile Tyr Asp Thr Phe
370 375 380

Gly Thr Ile Asp Glu Leu Glu Leu Phe Thr Ser Ala Ile Lys Arg Trp
385 390 395 400

Asn Ser Ser Glu Ile Glu His Leu Pro Glu Tyr Met Lys Cys Val Tyr
405 410 415

Met Val Val Phe Glu Thr Val Asn Glu Leu Thr Arg Glu Ala Glu Lys
420 425 430

Thr Gln Gly Arg Asn Thr Leu Asn Tyr Val Arg Lys Ala Trp Glu Ala
435 440 445

Tyr Phe Asp Ser Tyr Met Glu Glu Ala Lys Trp Ile Ser Asn Gly Tyr
450 455 460

Leu Pro Thr Phe Glu Glu Tyr His Glu Asn Gly Lys Val Ser Ser Ala
465 470 475 480

Tyr Arg Val Ala Thr Leu Gln Pro Ile Leu Thr Leu Asn Ala Trp Leu
485 490 495

Pro Asp Tyr Ile Leu Lys Gly Ile Asp Phe Pro Ser Arg Phe Asn Asp
500 505 510

Leu Ala Ser Ser Phe Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys
515 520 525

Ala Asp Arg Asp Arg Gly Glu Ala Ser Cys Ile Ser Cys Tyr Met
530 535 540

Lys Asp Asn Pro Gly Ser Thr Glu Glu Asp Ala Leu Asn His Ile Asn
545 550 555 560

Ala Met Val Asn Asp Ile Ile Lys Glu Leu Asn Trp Glu Leu Leu Arg
565 570 575

Ser Asn Asp Asn Ile Pro Met Leu Ala Lys Lys His Ala Phe Asp Ile
580 585 590

Thr Arg Ala Leu His His Leu Tyr Ile Tyr Arg Asp Gly Phe Ser Val
595 600 605

Ala Asn Lys Glu Thr Lys Lys Leu Val Met Glu Thr Leu Leu Glu Ser

610

615

620

Met Leu Phe
625

<210> 33
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR
oligonucleotide primer 2.2 BamHI

<400> 33
caaaggatc cagaatggct ctgg

24

<210> 34
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR
oligonucleotide primer 2.2 Not I

<400> 34
agtaaggccc cgctttttaa tcataccac

30

<210> 35
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR
oligonucleotide primer 3.18 EcoRI

<400> 35
ctgcaggaat tcggcacgag c

21

<210> 36
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR
oligonucleotide primer 3.18 SmaI

<400> 36
catagccccg ggcatacgatt tgagctg

27

<210> 37
<211> 30
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR
oligonucleotide primer 10 NdeI

<400> 37

ggcaggaaca tatggctctc ctttctatcg

30

<210> 38

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR
oligonucleotide primer 10 BamHI

<400> 38

tctagaacta gtggatcccc cgggctgcag

30

<210> 39

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR
oligonucleotide primer JB29

<400> 39

ctaccattcc aatatctg

18

<210> 40

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR
oligonucleotide primer 2-8

<400> 40

gttggatctt agaagttccc

20

<210> 41

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR
oligonucleotide primer 3-9

<400> 41

tttccattcc aacctctggg

20

<210> 42
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR
oligonucleotide primer 3-11

<400> 42
cgtaatggaa agctctggcg

20

<210> 43
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR
oligonucleotide primer 7-1

<400> 43
ccttacacgc ctttggatgg

20

<210> 44
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR
oligonucleotide sequence 7-3

<400> 44
tctgttgc caggatggtc

20

<210> 45
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: conserved
amino acid motif common to all prenyl transferases wherein Xaa at
position
3 and 4 represents any amino acid

<400> 45
Asp Asp Xaa Xaa Asp
1 5

<210> 46
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid motif from which oligonucleotide primers can be synthesized that hybridize to the monoterpene synthases of the present invention, wherein Xaa at position 4 represents
Leu or Ile or Val

<400> 46
His Ser Asn Xaa Trp Asp Asp Asp
1 5

<210> 47
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid motif from which degenerate oligonucleotides can be constructed that hybridize to the monoterpene synthases of the present invention

<400> 47
Ala Leu Asp Tyr Val Tyr
1 5

<210> 48
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid motif from which degenerate oligonucleotide sequences can be constructed that hybridize to the monoterpene synthases of the present invention

<400> 48
Glu Leu Ala Lys Leu Glu Phe
1 5

<210> 49
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid motif from which degenerate oligonucleotide sequences can be constructed that hybridize to monoterpene synthase clones of the present invention

<400> 49
Arg Trp Trp Lys Glu Ser
1 5

<210> 50
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid motif from which oligonucleotide sequences can be constructed that hybridize to monoterpane synthase clones of the present invention, wherein Xaa at position 1 represents Val or Ile or Leu

<400> 50
Xaa Leu Asp Asp Met Tyr Asp
1 5

<210> 51
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid motif from which oligonucleotide sequences can be constructed that hybridize to monoterpane synthase clones of the present invention wherein Xaa at position 1 represents Val or Ile or Leu

<400> 51
Xaa Leu Asp Asp Leu Tyr Asp
1 5

<210> 52
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid motif from which oligonucleotide sequences can be constructed that hybridize to the monoterpane synthase clones of the present invention, wherein Xaa at position 1 represents Val or Ile or Leu

<400> 52
Xaa Leu Asp Asp Ile Tyr Asp
1 5

<210> 53
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid

motif from which oligonucleotide sequences can be constructed that hybridize to the monoterpene synthase clones of the present invention, wherein Xaa at position 6 represents Asn or His

<400> 53
Cys Tyr Met Lys Asp Xaa Pro
1 5

<210> 54
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: exemplary oligonucleotide that corresponds to peptide sequence MetMetMet

<400> 54
atgatgtatg

9

<210> 55
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: exemplary oligonucleotide sequence that corresponds to peptide sequence MetMetMet

<400> 55
tactactac

9

<210> 56
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: exemplary oligonucleotide that corresponds to peptide sequence MetMetMet, n is inosine

<400> 56
nacnacnacnac

9

<210> 57
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide corresponding to amino acid
sequence set forth in SEQ ID NO:46

<220>
<221> misc_feature
<222> (1)..(24)
<223> Oligonucleotide that corresponds to the conserved
amino acid sequence set forth in SEQ ID NO:46

<400> 57
gtgtcggttgg agaccctgct gctg

24

<210> 58
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide sequence corresponding to amino
acid sequence set forth in SEQ ID NO:47

<220>
<221> misc_feature
<222> (1)..(18)
<223> Oligonucleotide corresponding to amino acid
sequence set forth in SEQ ID NO:47

<400> 58
cgggagctga tgcagatg

18

<210> 59
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide that corresponds to amino acid
sequence set forth in SEQ ID NO:48

<220>
<221> misc_feature
<222> (1)..(21)
<223> Oligonucleotide that corresponds to conserved
amino acid sequence set forth in SEQ ID NO:48

<400> 59
ctcgagcggt tcgagctcaa g

21

<210> 60
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide that corresponds to amino acid
sequence set forth in SEQ ID NO:49

<220>
<221> misc_feature
<222> (1)..(18)
<223> Oligonucleotide that corresponds to conserved
amino acid sequence set forth in SEQ ID NO:49

<400> 60
gccaccacct tcctctcg

18

<210> 61
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide sequence corresponding to amino
acid sequence set forth in SEQ ID NO:50

<220>
<221> misc_feature
<222> (1)..(21)
<223> Oligonucleotide sequence corresponding to amino
acid sequence set forth in SEQ ID NO:50

<400> 61
gaggagctgc tgtacatgct g

21

<210> 62
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide corresponding to amino acid
sequence set forth in SEQ ID NO:51

<220>
<221> misc_feature
<222> (1)..(21)
<223> Oligonucleotide corresponding to conserved amino
acid sequence set forth in SEQ ID NO:51

<400> 62
gaggagctgc tggagatgct g

21

<210> 63
<211> 293
<212> DNA
<213> Abies grandis

<400> 63
cttaatgaat tggcgcaaga ggctgagaag actcaaggca gagatacgct caacttatatt 60

cgcaatgctt atgagtctca ttttgattcg tttatgcacg aagcaaaatg gatctcaagt 120

ggttatctcc caacgttga ggagtacttg aagaatggga aagtttagttc cggttctcg 180
acagccactt tacaacccat actcaccttg gatgtaccac ttccctaatta catactgcaa 240
gaaattgatt atccatctag gttcaatgac ttggcttcgt ccctccctcg cta 293

<210> 64
<211> 2013
<212> DNA
<213> Abies grandis

<220>
<221> CDS
<222> (36)..(1889)

<400> 64
tttgacgtg ctttcttatac tgatagcaag ctgaa atg gct ctt ctt tct att 53
Met Ala Leu Leu Ser Ile
1 5

act ccg ctg gtt tcc agg tcg tgc ctc agt tct tct cat gag att aag 101
Thr Pro Leu Val Ser Arg Ser Cys Leu Ser Ser His Glu Ile Lys
10 15 20

gct ctc cgt aga aca atc cca act ctt gga atc tgc agg ccg ggg aaa 149
Ala Leu Arg Arg Thr Ile Pro Thr Leu Gly Ile Cys Arg Pro Gly Lys
25 30 35

tcc gtc gcg cat tcc ata aac atg tgt ttg aca agc gtc gca tct act 197
Ser Val Ala His Ser Ile Asn Met Cys Leu Thr Ser Val Ala Ser Thr
40 45 50

gat tct gta cag aga cgc gtg ggc aac tat cat tcc aac ctg tgg gac 245
Asp Ser Val Gln Arg Arg Val Gly Asn Tyr His Ser Asn Leu Trp Asp
55 60 65 70

gat gat ttc ata cag tct ctg atc tca acg cct tat gga gca cct gat 293
Asp Asp Phe Ile Gln Ser Leu Ile Ser Thr Pro Tyr Gly Ala Pro Asp
75 80 85

tac cgg gaa cgt gct gac aga ctt att ggg gaa gta aag gat ata atg 341
Tyr Arg Glu Arg Ala Asp Arg Leu Ile Gly Glu Val Lys Asp Ile Met
90 95 100

ttc aat ttc aag tcg ctg gaa gat gga ggc aat gat ctc ctt caa cga 389
Phe Asn Phe Lys Ser Leu Glu Asp Gly Gly Asn Asp Leu Leu Gln Arg
105 110 115

ctt ttg ctg gtc gat gac gtt gaa cgt ttg gga atc gac agg cat ttc 437
Leu Leu Leu Val Asp Asp Val Glu Arg Leu Gly Ile Asp Arg His Phe
120 125 130

aaa aaa gag ata aaa acg gca ctc gat tat gtt aac agt tat tgg aac 485
Lys Lys Glu Ile Lys Thr Ala Leu Asp Tyr Val Asn Ser Tyr Trp Asn
135 140 145 150

gaa aaa ggc att gga tgt ggg agg gag agt gtt gtg act gac ctc aac 533
Glu Lys Gly Ile Gly Cys Gly Arg Glu Ser Val Val Thr Asp Leu Asn
155 160 165

tca acc gcc ttg ggg ctt cga act ctc cga cta cac gga tac act gtg 581
Ser Thr Ala Leu Gly Leu Arg Thr Leu Arg Leu His Gly Tyr Thr Val
170 175 180

tct tca gat gtt ttg aac gtt ttt aaa gac aaa aat ggg caa ttt tcc 629
Ser Ser Asp Val Leu Asn Val Phe Lys Asp Lys Asn Gly Gln Phe Ser
185 190 195

tcc act gcc aat att cag ata gag gga gag att aga ggc gtt ctc aat 677
Ser Thr Ala Asn Ile Gln Ile Glu Gly Glu Ile Arg Gly Val Leu Asn
200 205 210

tta ttc agg gcc tcc ctc gtc gcc ttt ccc ggc gag aaa gtt atg gat 725
Leu Phe Arg Ala Ser Leu Val Ala Phe Pro Gly Glu Lys Val Met Asp
215 220 225 230

gaa gct gaa aca ttc tct aca aaa tat tta aga gaa gcc ctg caa aag 773
Glu Ala Glu Thr Phe Ser Thr Lys Tyr Leu Arg Glu Ala Leu Gln Lys
235 240 245

att ccg gca tcc agt ata ctt tca cta gag ata cgg gac gtt ctg gaa 821
Ile Pro Ala Ser Ser Ile Leu Ser Leu Glu Ile Arg Asp Val Leu Glu
250 255 260

tat ggt tgg cac acc aat ttg cca cgc ttg gaa gca agg aat tac atg 869
Tyr Gly Trp His Thr Asn Leu Pro Arg Leu Ala Arg Asn Tyr Met
265 270 275

gac gtc ttt gga cag cac act aaa aat aag aac gcc gcc gag aaa ctt 917
Asp Val Phe Gly Gln His Thr Lys Asn Ala Ala Glu Lys Leu
280 285 290

tta gaa ctt gca aaa ttg gaa ttc aat ata ttt cac tcc tta caa gag 965
Leu Glu Leu Ala Lys Leu Glu Phe Asn Ile Phe His Ser Leu Gln Glu
295 300 305 310

aga gag tta aaa cat gtt tcc cga tgg tgg aaa gac tcg ggt tct cct 1013
Arg Glu Leu Lys His Val Ser Arg Trp Trp Lys Asp Ser Gly Ser Pro
315 320 325

gag atg acc ttc tgt cga cat cgt cac gtg gaa tac tac gct ttg gct 1061
Glu Met Thr Phe Cys Arg His Arg His Val Glu Tyr Tyr Ala Leu Ala
330 335 340

tcc tgc att gcg ttc gag cct caa cat tct gga ttc aga ctc ggc ttt 1109
Ser Cys Ile Ala Phe Glu Pro Gln His Ser Gly Phe Arg Leu Gly Phe
345 350 355

acc aag atg tct cat ctt atc acg gtt ctt gac gac atg tac gac gtc 1157
Thr Lys Met Ser His Leu Ile Thr Val Leu Asp Asp Met Tyr Asp Val
360 365 370

ttc ggc aca gta gac gag ctg gaa ctc ttc aca gcg aca att aag aga 1205
Phe Gly Thr Val Asp Glu Leu Glu Leu Phe Thr Ala Thr Ile Lys Arg
375 380 385 390

tgg gat ccg tcc qcg atg gaa tgc ctt cca gaa tat atg aaa gga gtg 1253
Trp Asp Pro Ser Ala Met Glu Cys Leu Pro Glu Tyr Met Lys Gly Val
395 400 405

tac atg atg gtt tat cac acc gta aat gaa atg gct cga gtg gca gag 1301

Tyr Met Met Val Tyr His Thr Val Asn Glu Met Ala Arg Val Ala Glu
410 415 420

aag gct caa ggc cga gac acg ctc aac tat gca aga cag gct tgg gag 1349
Lys Ala Gln Gly Arg Asp Thr Leu Asn Tyr Ala Arg Gln Ala Trp Glu
425 430 435

gcg tgt ttt gat tcg tat atg cag gaa gca aag tgg atc gcc act ggt 1397
Ala Cys Phe Asp Ser Tyr Met Gln Glu Ala Lys Trp Ile Ala Thr Gly
440 445 450

tat ctg ccc acg ttt gag gag tac ttg gag aac ggg aaa gtt agc tct 1445
Tyr Leu Pro Thr Phe Glu Glu Tyr Leu Glu Asn Gly Lys Val Ser Ser
455 460 465 470

gct cat cgc cca tgc gca ctg caa ccc att ctg acg ttg gac atc ccc 1493
Ala His Arg Pro Cys Ala Leu Gln Pro Ile Leu Thr Leu Asp Ile Pro
475 480 485

ttt cct gat cac atc ctc aag gaa gtt gac ttc cca tcg aag ctc aat 1541
Phe Pro Asp His Ile Leu Lys Glu Val Asp Phe Pro Ser Lys Leu Asn
490 495 500

gac ttg ata tgt atc atc ctt cga tta aga ggt gat aca cgg tgc tac 1589
Asp Leu Ile Cys Ile Ile Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr
505 510 515

aag gca gac agg gcc cgt gga gaa gaa gct tcg tct ata tca tgt tat 1637
Lys Ala Asp Arg Ala Arg Gly Glu Glu Ala Ser Ser Ile Ser Cys Tyr
520 525 530

atg aaa gac aat cct gga tta acg gaa gaa gat gct ctg aat cat atc 1685
Met Lys Asp Asn Pro Gly Leu Thr Glu Glu Asp Ala Leu Asn His Ile
535 540 545 550

aac ttc atg atc agg gac gca atc aga gaa tta aat tgg gag ctt cta 1733
Asn Phe Met Ile Arg Asp Ala Ile Arg Glu Leu Asn Trp Glu Leu Leu
555 560 565

aag cca gac aac agt gtt ccc atc act tcc aag aaa cac gca ttt gac 1781
Lys Pro Asp Asn Ser Val Pro Ile Thr Ser Lys Lys His Ala Phe Asp
570 575 580

ata agc aga gtt tgg cat cac ggt tac aga tac cga gat ggc tac agc 1829
Ile Ser Arg Val Trp His His Gly Tyr Arg Tyr Arg Asp Gly Tyr Ser
585 590 595

ttt gcc aac gtt gaa aca aag agt ttg gtg atg aga acc gtc att gaa 1877
Phe Ala Asn Val Glu Thr Lys Ser Leu Val Met Arg Thr Val Ile Glu
600 605 610

cct gtg cct ttg taacaacact tcaaattctac aatattaact gaggatgccc 1929
Pro Val Pro Leu
615

tatgggtgta tatagggcac acaaaaataa atatggttgt gtttagtaaag ctgtaattta 1989

taaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa aaaa 2013

<211> 618

<212> PRT

<213> Abies grandis

<400> 65

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Ser Ser His Glu Ile Lys Ala Leu Arg Arg Thr Ile Pro Thr Leu Gly
20 25 30

Ile Cys Arg Pro Gly Lys Ser Val Ala His Ser Ile Asn Met Cys Leu
35 40 45

Thr Ser Val Ala Ser Thr Asp Ser Val Gln Arg Arg Val Gly Asn Tyr
50 55 60

His Ser Asn Leu Trp Asp Asp Asp Phe Ile Gln Ser Leu Ile Ser Thr
65 70 75 80

Pro Tyr Gly Ala Pro Asp Tyr Arg Glu Arg Ala Asp Arg Leu Ile Gly
85 90 95

Glu Val Lys Asp Ile Met Phe Asn Phe Lys Ser Leu Glu Asp Gly Gly
100 105 110

Asn Asp Leu Leu Gln Arg Leu Leu Val Asp Asp Val Glu Arg Leu
115 120 125

Gly Ile Asp Arg His Phe Lys Lys Glu Ile Lys Thr Ala Leu Asp Tyr
130 135 140

Val Asn Ser Tyr Trp Asn Glu Lys Gly Ile Gly Cys Gly Arg Glu Ser
145 150 155 160

Val Val Thr Asp Leu Asn Ser Thr Ala Leu Gly Leu Arg Thr Leu Arg
165 170 175

Leu His Gly Tyr Thr Val Ser Ser Asp Val Leu Asn Val Phe Lys Asp
180 185 190

Lys Asn Gly Gln Phe Ser Ser Thr Ala Asn Ile Gln Ile Glu Gly Glu
195 200 205

Ile Arg Gly Val Leu Asn Leu Phe Arg Ala Ser Leu Val Ala Phe Pro
210 215 220

Gly Glu Lys Val Met Asp Glu Ala Glu Thr Phe Ser Thr Lys Tyr Leu
225 230 235 240

Arg Glu Ala Leu Gln Lys Ile Pro Ala Ser Ser Ile Leu Ser Leu Glu
245 250 255

Ile Arg Asp Val Leu Glu Tyr Gly Trp His Thr Asn Leu Pro Arg Leu
260 265 270

Glu Ala Arg Asn Tyr Met Asp Val Phe Gly Gln His Thr Lys Asn Lys
275 280 285

Asn Ala Ala Glu Lys Leu Leu Glu Leu Ala Lys Leu Glu Phe Asn Ile
290 295 300

Phe His Ser Leu Gln Glu Arg Glu Leu Lys His Val Ser Arg Trp Trp
305 310 315 320

Lys Asp Ser Gly Ser Pro Glu Met Thr Phe Cys Arg His Arg His Val
325 330 335

Glu Tyr Tyr Ala Leu Ala Ser Cys Ile Ala Phe Glu Pro Gln His Ser
340 345 350

Gly Phe Arg Leu Gly Phe Thr Lys Met Ser His Leu Ile Thr Val Leu
355 360 365

Asp Asp Met Tyr Asp Val Phe Gly Thr Val Asp Glu Leu Glu Leu Phe
370 375 380

Thr Ala Thr Ile Lys Arg Trp Asp Pro Ser Ala Met Glu Cys Leu Pro
385 390 395 400

Glu Tyr Met Lys Gly Val Tyr Met Met Val Tyr His Thr Val Asn Glu
405 410 415

Met Ala Arg Val Ala Glu Lys Ala Gln Gly Arg Asp Thr Leu Asn Tyr
420 425 430

Ala Arg Gln Ala Trp Glu Ala Cys Phe Asp Ser Tyr Met Gln Glu Ala
435 440 445

Lys Trp Ile Ala Thr Gly Tyr Leu Pro Thr Phe Glu Glu Tyr Leu Glu
450 455 460

Asn Gly Lys Val Ser Ser Ala His Arg Pro Cys Ala Leu Gln Pro Ile
465 470 475 480

Leu Thr Leu Asp Ile Pro Phe Pro Asp His Ile Leu Lys Glu Val Asp
485 490 495

Phe Pro Ser Lys Leu Asn Asp Leu Ile Cys Ile Ile Leu Arg Leu Arg
500 505 510

Gly Asp Thr Arg Cys Tyr Lys Ala Asp Arg Ala Arg Gly Glu Glu Ala
515 520 525

Ser Ser Ile Ser Cys Tyr Met Lys Asp Asn Pro Gly Leu Thr Glu Glu
530 535 540

Asp Ala Leu Asn His Ile Asn Phe Met Ile Arg Asp Ala Ile Arg Glu
545 550 555 560

Leu Asn Trp Glu Leu Leu Lys Pro Asp Asn Ser Val Pro Ile Thr Ser
565 570 575

Lys Lys His Ala Phe Asp Ile Ser Arg Val Trp His His Gly Tyr Arg
580 585 590

Tyr Arg Asp Gly Tyr Ser Phe Ala Asn Val Glu Thr Lys Ser Leu Val
595 600 605

Met Arg Thr Val Ile Glu Pro Val Pro Leu
610 615

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<213> Abies grandis

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<400> 66

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ccc aaa tcc tgc ctg cac aaa tcg ttg atc agg tct act cat cat gag 102
Pro Lys Ser Cys Leu His Lys Ser Leu Ile Arg Ser Thr His His Glu
10 15 20

ctc aag cct ctg cgc aga acc atc cca act ctt gga atg tgt agg cga 150
Leu Lys Pro Leu Arg Arg Thr Ile Pro Thr Leu Gly Met Cys Arg Arg
25 30 35

ggg aaa tct ttc aca cct tct gtg agc atg agt ttg acc acc gct gta 198
Gly Lys Ser Phe Thr Pro Ser Val Ser Met Ser Leu Thr Thr Ala Val
40 45 50 55

tct gat gat ggt cta caa aga cgc ata ggt gac tat cat tcc aat ctc 246
Ser Asp Asp Gly Leu Gln Arg Arg Ile Gly Asp Tyr His Ser Asn Leu
60 65 70

tgg gac gac gat ttc ata cag tct cta tca acg cct tat ggg gag cct 294
Trp Asp Asp Asp Phe Ile Gln Ser Leu Ser Thr Pro Tyr Gly Glu Pro
75 80 85

tct tac cga gaa cgt gct gag aaa ctg att ggg gaa gtg aag gag atg 342
Ser Tyr Arg Glu Arg Ala Glu Lys Leu Ile Gly Glu Val Lys Glu Met
90 95 100

ttc aat tca atg cca tcg gaa gat gga gaa tca atg agt ccc ctc aat 390
Phe Asn Ser Met Pro Ser Glu Asp Gly Glu Ser Met Ser Pro Leu Asn
105 110 115

gat ctt att gaa cga ctt tgg atg gtc gat agc gtt gaa cgt ttg ggg 438
Asp Leu Ile Glu Arg Leu Trp Met Val Asp Ser Val Glu Arg Leu Gly
120 125 130 135

att gat aga cat ttc aaa aaa gag ata aaa tca gcc ctt gat tat gtt 486
Ile Asp Arg His Phe Lys Lys Glu Ile Lys Ser Ala Leu Asp Tyr Val
140 145 150

tac agt tat tgg aac gaa aaa ggt att gga tgc ggt aga gat agt gtt 534
Tyr Ser Tyr Trp Asn Glu Lys Gly Ile Gly Cys Gly Arg Asp Ser Val
155 160 165

ttt cct gat gtc aac tcg act gcc tcg ggg ttt cga act ctt cgc cta 582
Phe Pro Asp Val Asn Ser Thr Ala Ser Gly Phe Arg Thr Leu Arg Leu
170 175 180

cac gga tac agt gtc tct tca gag gtt ttg aaa gta ttt caa gac caa 630
His Gly Tyr Ser Val Ser Glu Val Leu Lys Val Phe Gln Asp Gln

185	190	195	
aat ggg cag ttt gca ttc tct cct agt aca aaa gag aga gac atc aga Asn Gly Gln Phe Ala Phe Ser Pro Ser Thr Lys Glu Arg Asp Ile Arg 200 205 210 215			678
acc gtt ctg aat tta tat cgg gct tct ttc att gcc ttt cct ggg gag Thr Val Leu Asn Leu Tyr Arg Ala Ser Phe Ile Ala Phe Pro Gly Glu 220 225 230			726
aaa gtt atg gaa gag gct gaa att ttc tct tca aga tat ttg aaa gaa Lys Val Met Glu Glu Ala Glu Ile Phe Ser Ser Arg Tyr Leu Lys Glu 235 240 245			774
gcc gtg caa aag att ccg gtc tcc agt ctt tca caa gaa ata gac tac Ala Val Gln Lys Ile Pro Val Ser Ser Leu Ser Gln Glu Ile Asp Tyr 250 255 260			822
act ttg gaa tat ggt tgg cac aca aat atg cca aga ttg gaa aca agg Thr Leu Glu Tyr Gly Trp His Thr Asn Met Pro Arg Leu Glu Thr Arg 265 270 275			870
aat tac tta gat gta ttt gga cat cct acc agt cca tgg ctc aag aag Asn Tyr Leu Asp Val Phe Gly His Pro Thr Ser Pro Trp Leu Lys Lys 280 285 290 295			918
aaa agg acg caa tat ctg gac agc gaa aag ctt tta gaa ctc gca aaa Lys Arg Thr Gln Tyr Leu Asp Ser Glu Lys Leu Leu Glu Leu Ala Lys 300 305 310			966
ttg gag ttc aac atc ttt cac tcc ctt caa cag aag gag tta cag tat Leu Glu Phe Asn Ile Phe His Ser Leu Gln Gln Lys Glu Leu Gln Tyr 315 320 325			1014
ctc tcc aga tgg tgg ata cat tcg ggt ttg cct gaa ctg acc ttt ggt Leu Ser Arg Trp Trp Ile His Ser Gly Leu Pro Glu Leu Thr Phe Gly 330 335 340			1062
cgg cat cgt cac gtg gaa tac tac acc ctg agc tct tgc att gcg act Arg His Arg His Val Glu Tyr Tyr Thr Leu Ser Ser Cys Ile Ala Thr 345 350 355			1110
gag ccc aaa cat tct gca ttc aga ttg ggc ttt gcc aaa acg tgt cat Glu Pro Lys His Ser Ala Phe Arg Leu Gly Phe Ala Lys Thr Cys His 360 365 370 375			1158
ctt atc acg gtt ctg gac gat atc tac gac act ttc gga acg atg gat Leu Ile Thr Val Leu Asp Asp Ile Tyr Asp Thr Phe Gly Thr Met Asp 380 385 390			1206
gaa atc gaa ctc ttc aac gag gca gtt agg aga tgg aat ccg tcg gag Glu Ile Glu Leu Phe Asn Glu Ala Val Arg Arg Trp Asn Pro Ser Glu 395 400 405			1254
aaa gaa cgc ctc cca gaa tat atg aaa gaa atc tac atg gca ctc tac Lys Glu Arg Leu Pro Glu Tyr Met Lys Glu Ile Tyr Met Ala Leu Tyr 410 415 420			1302
gaa gcc tta act gac atg gcg cga gag gca gag aag aca caa ggc cga Glu Ala Leu Thr Asp Met Ala Arg Glu Ala Glu Lys Thr Gln Gly Arg 425 430 435			1350

gac acg ctc aat tat gct aga aag gct tgg gaa gtt tat ctt gat tcg 1398
Asp Thr Leu Asn Tyr Ala Arg Lys Ala Trp Glu Val Tyr Leu Asp Ser
440 445 450 455

tat aca caa gaa gca aag tgg atc gcc agc ggt tat ctg cca act ttc 1446
Tyr Thr Gln Glu Ala Lys Trp Ile Ala Ser Gly Tyr Leu Pro Thr Phe
460 465 470

gag gag tac tta gag aac gcg aag gtt agc tct ggt cat cgt gca gcg 1494
Glu Glu Tyr Leu Glu Asn Ala Lys Val Ser Ser Gly His Arg Ala Ala
475 480 485

gca ttg aca ccc ctc ctg aca ttg gac gta ccg ctt cct gat gac gtc 1542
Ala Leu Thr Pro Leu Leu Thr Leu Asp Val Pro Leu Pro Asp Asp Val
490 495 500

ttg aag gga ata gat ttt cca tcg aga ttt aat gat ttg gca tct tcc 1590
Leu Lys Gly Ile Asp Phe Pro Ser Arg Phe Asn Asp Leu Ala Ser Ser
505 510 515

ttc ctt aga cta aga ggt gac aca cga tgc tac aag gca gac agg gac 1638
Phe Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys Ala Asp Arg Asp
520 525 530 535

cga gga gaa gaa gcg tca agc ata tcg tgt tac atg aaa gac aat ccc 1686
Arg Gly Glu Ala Ser Ser Ile Ser Cys Tyr Met Lys Asp Asn Pro
540 545 550

gga tta aca gag gaa gat gct ctc aat cat atc aat gcc atg atc aac 1734
Gly Leu Thr Glu Glu Asp Ala Leu Asn His Ile Asn Ala Met Ile Asn
555 560 565

gac ata atc aaa gaa tta aat tgg gaa ctt ctc aaa ccc gat agc aat 1782
Asp Ile Ile Lys Glu Leu Asn Trp Glu Leu Leu Lys Pro Asp Ser Asn
570 575 580

att cca atg act gca cg^g aaa cat gct tat gag ata acc aga gct ttc 1830
Ile Pro Met Thr Ala Arg Lys His Ala Tyr Glu Ile Thr Arg Ala Phe
585 590 595

cac caa ctt tac aaa tat aga gat ggc ttc agc gtt gcc act caa gaa 1878
His Gln Leu Tyr Lys Tyr Arg Asp Gly Phe Ser Val Ala Thr Gln Glu
600 605 610 615

acg aaa agt ttg gtg agg aga acg gtc ctt gaa cca gtg cct ctt 1923
Thr Lys Ser Leu Val Arg Arg Thr Val Leu Glu Pro Val Pro Leu
620 625 630

taacaattta aacttctat aataaattgg tggatgtcc gctatgcgtt tatgcatttg 1983

catgtctctc tatgtacta gtttatgtcg tggatgtattt ataaaattgg aggttactcg 2043

gtcctcacat ggtatatgt gagttgtgaa attctaaaaaaa aaaaaaaaaaaa aaaaaaaaaa 2103

aaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa 2163

aaaaaaaaaaa aaaaaaaaaaaa aaa 2186

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<213> Abies grandis

<400> 67
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Thr Leu Gly Met Cys Arg Arg Gly Lys Ser Phe Thr Pro Ser Val Ser
35 40 45
Met Ser Leu Thr Thr Ala Val Ser Asp Asp Gly Leu Gln Arg Arg Ile
50 55 60
Gly Asp Tyr His Ser Asn Leu Trp Asp Asp Asp Phe Ile Gln Ser Leu
65 70 75 80
Ser Thr Pro Tyr Gly Glu Pro Ser Tyr Arg Glu Arg Ala Glu Lys Leu
85 90 95
Ile Gly Glu Val Lys Glu Met Phe Asn Ser Met Pro Ser Glu Asp Gly
100 105 110
Glu Ser Met Ser Pro Leu Asn Asp Leu Ile Glu Arg Leu Trp Met Val
115 120 125
Asp Ser Val Glu Arg Leu Gly Ile Asp Arg His Phe Lys Lys Glu Ile
130 135 140
Lys Ser Ala Leu Asp Tyr Val Tyr Ser Tyr Trp Asn Glu Lys Gly Ile
145 150 155 160
Gly Cys Gly Arg Asp Ser Val Phe Pro Asp Val Asn Ser Thr Ala Ser
165 170 175
Gly Phe Arg Thr Leu Arg Leu His Gly Tyr Ser Val Ser Ser Glu Val
180 185 190
Leu Lys Val Phe Gln Asp Gln Asn Gly Gln Phe Ala Phe Ser Pro Ser
195 200 205
Thr Lys Glu Arg Asp Ile Arg Thr Val Leu Asn Leu Tyr Arg Ala Ser
210 215 220
Phe Ile Ala Phe Pro Gly Glu Lys Val Met Glu Glu Ala Glu Ile Phe
225 230 235 240
Ser Ser Arg Tyr Leu Lys Glu Ala Val Gln Lys Ile Pro Val Ser Ser
245 250 255
Leu Ser Gln Glu Ile Asp Tyr Thr Leu Glu Tyr Gly Trp His Thr Asn
260 265 270
Met Pro Arg Leu Glu Thr Arg Asn Tyr Leu Asp Val Phe Gly His Pro
275 280 285
Thr Ser Pro Trp Leu Lys Lys Lys Arg Thr Gln Tyr Leu Asp Ser Glu
290 295 300

Lys Leu Leu Glu Leu Ala Lys Leu Glu Phe Asn Ile Phe His Ser Leu
305 310 315 320

Gln Gln Lys Glu Leu Gln Tyr Leu Ser Arg Trp Trp Ile His Ser Gly
325 330 335

Leu Pro Glu Leu Thr Phe Gly Arg His Arg His Val Glu Tyr Tyr Thr
340 345 350

Leu Ser Ser Cys Ile Ala Thr Glu Pro Lys His Ser Ala Phe Arg Leu
355 360 365

Gly Phe Ala Lys Thr Cys His Leu Ile Thr Val Leu Asp Asp Ile Tyr
370 375 380

Asp Thr Phe Gly Thr Met Asp Glu Ile Glu Leu Phe Asn Glu Ala Val
385 390 395 400

Arg Arg Trp Asn Pro Ser Glu Lys Glu Arg Leu Pro Glu Tyr Met Lys
405 410 415

Glu Ile Tyr Met Ala Leu Tyr Glu Ala Leu Thr Asp Met Ala Arg Glu
420 425 430

Ala Glu Lys Thr Gln Gly Arg Asp Thr Leu Asn Tyr Ala Arg Lys Ala
435 440 445

Trp Glu Val Tyr Leu Asp Ser Tyr Thr Gln Glu Ala Lys Trp Ile Ala
450 455 460

Ser Gly Tyr Leu Pro Thr Phe Glu Glu Tyr Leu Glu Asn Ala Lys Val
465 470 475 480

Ser Ser Gly His Arg Ala Ala Leu Thr Pro Leu Leu Thr Leu Asp
485 490 495

Val Pro Leu Pro Asp Asp Val Leu Lys Gly Ile Asp Phe Pro Ser Arg
500 505 510

Phe Asn Asp Leu Ala Ser Ser Phe Leu Arg Leu Arg Gly Asp Thr Arg
515 520 525

Cys Tyr Lys Ala Asp Arg Asp Arg Gly Glu Glu Ala Ser Ser Ile Ser
530 535 540

Cys Tyr Met Lys Asp Asn Pro Gly Leu Thr Glu Glu Asp Ala Leu Asn
545 550 555 560

His Ile Asn Ala Met Ile Asn Asp Ile Ile Lys Glu Leu Asn Trp Glu
565 570 575

Leu Leu Lys Pro Asp Ser Asn Ile Pro Met Thr Ala Arg Lys His Ala
580 585 590

Tyr Glu Ile Thr Arg Ala Phe His Gln Leu Tyr Lys Tyr Arg Asp Gly
595 600 605

Phe Ser Val Ala Thr Gln Glu Thr Lys Ser Leu Val Arg Arg Thr Val
610 615 620

Leu Glu Pro Val Pro Leu
625 630

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<211> 2429
<212> DNA
<213> Abies grandis

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<221> CDS
<222> (35)..(1945)

<400> 68
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Ser Leu Gln Val Pro Lys Ser Cys Gly Leu Lys Ser Leu Ile Ser Ser
10 15 20

agc aat gtg cag aag gct ctc tgt atc tct aca gca gtc cca act ctc 151
Ser Asn Val Gln Lys Ala Leu Cys Ile Ser Thr Ala Val Pro Thr Leu
25 30 35

aga atg cgt agg cga cag aaa gct ctg gtc atc aac atg aaa ttg acc 199
Arg Met Arg Arg Arg Gln Lys Ala Leu Val Ile Asn Met Lys Leu Thr
40 45 50 55

act gta tcc cat cgt gat gat aat ggt ggt gta ctg caa aga cgc 247
Thr Val Ser His Arg Asp Asp Asn Gly Gly Val Leu Gln Arg Arg
60 65 70

ata gcc gat cat cat ccc aac ctg tgg gaa gat gat ttc ata caa tca 295
Ile Ala Asp His His Pro Asn Leu Trp Glu Asp Asp Phe Ile Gln Ser
75 80 85

ttg tcc tca cct tat ggg gga tct tcg tac agt gaa cgt gct gtg aca 343
Leu Ser Ser Pro Tyr Gly Gly Ser Ser Tyr Ser Glu Arg Ala Val Thr
90 95 100

gtg gtt gag gaa gta aaa gag atg ttc aat tca ata cca aat aat aga 391
Val Val Glu Glu Val Lys Glu Met Phe Asn Ser Ile Pro Asn Asn Arg
105 110 115

gaa tta ttt ggt tcc caa aat gat ctc ctt aca cgc ctt tgg atg gtg 439
Glu Leu Phe Gly Ser Gln Asn Asp Leu Leu Thr Arg Leu Trp Met Val
120 125 130 135

gat agc att gaa cgt ctg ggg ata gat aga cat ttc caa aat gag ata 487
Asp Ser Ile Glu Arg Leu Gly Ile Asp Arg His Phe Gln Asn Glu Ile
140 145 150

aga gta gcc ctc gat tat gtt tac agt tat tgg aag gaa aag gaa ggc 535
Arg Val Ala Leu Asp Tyr Val Tyr Ser Tyr Trp Lys Glu Lys Glu Gly
155 160 165

att ggg tgt ggc aga gat tct act ttt cct gat ctc aac tcg act gct 583
Ile Gly Cys Gly Arg Asp Ser Thr Phe Pro Asp Leu Asn Ser Thr Ala
170 175 180

ctg gcg ctt cga act ctt cga ctg cac gga tac aat gtg tct tca gat 631
Leu Ala Leu Arg Thr Leu Arg Leu His Gly Tyr Asn Val Ser Ser Asp
185 190 195

gtg ctg gaa tac ttc aaa gat caa aag ggg cat ttt gcc tgc cct gca 679
Val Leu Glu Tyr Phe Lys Asp Gln Lys Gly His Phe Ala Cys Pro Ala
200 205 210 215

atc cta acc gag gga cag atc act aga agt gtt cta aat tta tat cgg 727
Ile Leu Thr Glu Gly Gln Ile Thr Arg Ser Val Leu Asn Leu Tyr Arg
220 225 230

gct tcc ctg gtc gcc ttt ccg ggg gag aaa gtt atg gaa gag gct gaa 775
Ala Ser Leu Val Ala Phe Pro Gly Glu Lys Val Met Glu Glu Ala Glu
235 240 245

atc ttc tcg gca tct tat ttg aaa gaa gtc tta caa aag att cca gtc 823
Ile Phe Ser Ala Ser Tyr Leu Lys Glu Val Leu Gln Lys Ile Pro Val
250 255 260

tcc agt ttt tca cga gag ata gaa tac gtt ttg gaa tat ggt tgg cac 871
Ser Ser Phe Ser Arg Glu Ile Glu Tyr Val Leu Glu Tyr Gly Trp His
265 270 275

aca aat ttg cca aga ttg gaa gca aga aat tat atc gac gtc tac ggg 919
Thr Asn Leu Pro Arg Leu Glu Ala Arg Asn Tyr Ile Asp Val Tyr Gly
280 285 290 295

cag gac agc tat gaa agt tca aac gag atg cca tat gtg aat acg cag 967
Gln Asp Ser Tyr Glu Ser Ser Asn Glu Met Pro Tyr Val Asn Thr Gln
300 305 310

aag ctt tta aaa ctt gca aaa ttg gag ttt aat atc ttt cac tct ttg 1015
Lys Leu Leu Lys Leu Ala Lys Leu Glu Phe Asn Ile Phe His Ser Leu
315 320 325

caa cag aaa gag ttg caa tat atc tct aga tgg tgg aaa gat tcg tgt 1063
Gln Gln Lys Glu Leu Gln Tyr Ile Ser Arg Trp Trp Lys Asp Ser Cys
330 335 340

tca tct cat ctg act ttt act cga cac cgt cac gtg gaa tac tac aca 1111
Ser Ser His Leu Thr Phe Thr Arg His Arg His Val Glu Tyr Tyr Thr
345 350 355

atg gca tct tgc att tct atg gag ccg aaa cac tcc gct ttc aga ttg 1159
Met Ala Ser Cys Ile Ser Met Glu Pro Lys His Ser Ala Phe Arg Leu
360 365 370 375

ggg ttt gtc aaa aca tgt cat ctt cta aca gtt ctg gat gat atg tat 1207
Gly Phe Val Lys Thr Cys His Leu Leu Thr Val Leu Asp Asp Met Tyr
380 385 390

gac act ttt gga aca ctg gac gaa ctc caa ctt ttt acg act gcc ttt 1255
Asp Thr Phe Gly Thr Leu Asp Glu Leu Gln Leu Phe Thr Thr Ala Phe
395 400 405

aag aga tgg gat ttg tca gag aca aag tgt ctt cca gaa tat atg aaa 1303
Lys Arg Trp Asp Leu Ser Glu Thr Lys Cys Leu Pro Glu Tyr Met Lys
410 415 420

gca gtg tac atg gac ttg tat caa tgt ctt aat gaa ttg gcg caa gag 1351
Ala Val Tyr Met Asp Leu Tyr Gln Cys Leu Asn Glu Leu Ala Gln Glu
425 430 435

gct gag aag act caa ggc aga gat acg ctc aac tat att cgc aat gct 1399
Ala Glu Lys Thr Gln Gly Arg Asp Thr Leu Asn Tyr Ile Arg Asn Ala
440 445 450 455

tat gag tct cat ttt gat tcg ttt atg cac gaa gca aaa tgg atc tca 1447
Tyr Glu Ser His Phe Asp Ser Phe Met His Glu Ala Lys Trp Ile Ser
460 465 470

agt ggt tat ctc cca acg ttt gag gag tac ttg aag aat ggg aaa gtt 1495
Ser Gly Tyr Leu Pro Thr Phe Glu Glu Tyr Leu Lys Asn Gly Lys Val
475 480 485

agt tcc ggt tct cgc aca gcc act tta caa ccc ata ctc acc ttg gat 1543
Ser Ser Gly Ser Arg Thr Ala Thr Leu Gln Pro Ile Leu Thr Leu Asp
490 495 500

gta cca ctt cct aat tac ata ctg caa gaa att gat tat cca tct agg 1591
Val Pro Leu Pro Asn Tyr Ile Leu Gln Glu Ile Asp Tyr Pro Ser Arg
505 510 515

ttc aat gac ttg gct tcg tcc ctt cgg cta cgt ggt gac acg cgc 1639
Phe Asn Asp Leu Ala Ser Ser Leu Leu Arg Leu Arg Gly Asp Thr Arg
520 525 530 535

tgc tac aag gcg gat agg gct cgt gga gaa gaa gct tca gct ata tcg 1687
Cys Tyr Lys Ala Asp Arg Ala Arg Gly Glu Ala Ser Ala Ile Ser
540 545 550

tgt tat atg aaa gac cat cct gga tca aca gag gaa gat gct ctc aat 1735
Cys Tyr Met Lys Asp His Pro Gly Ser Thr Glu Glu Asp Ala Leu Asn
555 560 565

cat atc aac gtc atg atc agt gat gca atc aca gaa tta aat tgg gag 1783
His Ile Asn Val Met Ile Ser Asp Ala Ile Arg Glu Leu Asn Trp Glu
570 575 580

ctt ctc aga cca gat agc aaa agt ccc atc tct tcc aag aaa cat gct 1831
Leu Leu Arg Pro Asp Ser Lys Ser Pro Ile Ser Ser Lys Lys His Ala
585 590 595

ttt gac atc acc aga gct ttc cat cac ctc tac aag tac cga gat ggt 1879
Phe Asp Ile Thr Arg Ala Phe His His Leu Tyr Lys Tyr Arg Asp Gly
600 605 610 615

tac act gtt gcg agt agt gaa aca aag aat ttg gtg atg aaa aca gtt 1927
Tyr Thr Val Ala Ser Ser Glu Thr Lys Asn Leu Val Met Lys Thr Val
620 625 630

ctt gaa cct gtg gca ttg taaaaaaaata tcaaccgcac caaaaatgcac 1975
Leu Glu Pro Val Ala Leu
635

ggagtttgta atttaatgca cttcttttat aatacacttc tcttagacc tggatgtgaag 2035
ccgatgcacc attacagtgt atatgggagc cagtcgtatc tcaaaaagtt tgtaaatgtt 2095
attctatgat atactctta gaccaaaagc tagatgccca tgaaaagcaa gtgttttaga 2155

attgcttcgt gatttgctta aattttctcc atgattcttt agaaatgttg catccccaaa 2215
cttcaactgcc atataagata acgggagtga caaggatttt aaagaggatt ttttttatg 2275
tcccgcatca caaggttgt cgatttacag ttgtttcaa gactgaagta ggatttccac 2335
cctccattaa tcctcttctc gatgttata tag tttcaacttga gcttgtgtatg gaagtcaatt 2395
cctagatatt tataagaaaa aaaaaaaaaa aaaa 2429

<210> 69
<211> 637
<212> PRT
<213> Abies grandis

<400> 69
Met Ala Leu Leu Ser Ile Val Ser Leu Gln Val Pro Lys Ser Cys Gly
1 5 10 15

Leu Lys Ser Leu Ile Ser Ser Ser Asn Val Gln Lys Ala Leu Cys Ile
20 25 30

Ser Thr Ala Val Pro Thr Leu Arg Met Arg Arg Arg Gln Lys Ala Leu
35 40 45

Val Ile Asn Met Lys Leu Thr Thr Val Ser His Arg Asp Asp Asn Gly
50 55 60

Gly Gly Val Leu Gln Arg Arg Ile Ala Asp His His Pro Asn Leu Trp
65 70 75 80

Glu Asp Asp Phe Ile Gln Ser Leu Ser Ser Pro Tyr Gly Gly Ser Ser
85 90 95

Tyr Ser Glu Arg Ala Val Thr Val Val Glu Glu Val Lys Glu Met Phe
100 105 110

Asn Ser Ile Pro Asn Asn Arg Glu Leu Phe Gly Ser Gln Asn Asp Leu
115 120 125

Leu Thr Arg Leu Trp Met Val Asp Ser Ile Glu Arg Leu Gly Ile Asp
130 135 140

Arg His Phe Gln Asn Glu Ile Arg Val Ala Leu Asp Tyr Val Tyr Ser
145 150 155 160

Tyr Trp Lys Glu Lys Glu Gly Ile Gly Cys Gly Arg Asp Ser Thr Phe
165 170 175

Pro Asp Leu Asn Ser Thr Ala Leu Ala Leu Arg Thr Leu Arg Leu His
180 185 190

Gly Tyr Asn Val Ser Ser Asp Val Leu Glu Tyr Phe Lys Asp Gln Lys
195 200 205

Gly His Phe Ala Cys Pro Ala Ile Leu Thr Glu Gly Gln Ile Thr Arg
210 215 220

Ser Val Leu Asn Leu Tyr Arg Ala Ser Leu Val Ala Phe Pro Gly Glu

225	230	235	240
Lys Val Met Glu Glu Ala Glu Ile Phe Ser Ala Ser Tyr Leu Lys Glu			
245	250	255	
Val Leu Gln Lys Ile Pro Val Ser Ser Phe Ser Arg Glu Ile Glu Tyr			
260	265	270	
Val Leu Glu Tyr Gly Trp His Thr Asn Leu Pro Arg Leu Glu Ala Arg			
275	280	285	
Asn Tyr Ile Asp Val Tyr Gly Gln Asp Ser Tyr Glu Ser Ser Asn Glu			
290	295	300	
Met Pro Tyr Val Asn Thr Gln Lys Leu Leu Lys Leu Ala Lys Leu Glu			
305	310	315	320
Phe Asn Ile Phe His Ser Leu Gln Gln Lys Glu Leu Gln Tyr Ile Ser			
325	330	335	
Arg Trp Trp Lys Asp Ser Cys Ser Ser His Leu Thr Phe Thr Arg His			
340	345	350	
Arg His Val Glu Tyr Tyr Thr Met Ala Ser Cys Ile Ser Met Glu Pro			
355	360	365	
Lys His Ser Ala Phe Arg Leu Gly Phe Val Lys Thr Cys His Leu Leu			
370	375	380	
Thr Val Leu Asp Asp Met Tyr Asp Thr Phe Gly Thr Leu Asp Glu Leu			
385	390	395	400
Gln Leu Phe Thr Thr Ala Phe Lys Arg Trp Asp Leu Ser Glu Thr Lys			
405	410	415	
Cys Leu Pro Glu Tyr Met Lys Ala Val Tyr Met Asp Leu Tyr Gln Cys			
420	425	430	
Leu Asn Glu Leu Ala Gln Glu Ala Glu Lys Thr Gln Gly Arg Asp Thr			
435	440	445	
Leu Asn Tyr Ile Arg Asn Ala Tyr Glu Ser His Phe Asp Ser Phe Met			
450	455	460	
His Glu Ala Lys Trp Ile Ser Ser Gly Tyr Leu Pro Thr Phe Glu Glu			
465	470	475	480
Tyr Leu Lys Asn Gly Lys Val Ser Ser Gly Ser Arg Thr Ala Thr Leu			
485	490	495	
Gln Pro Ile Leu Thr Leu Asp Val Pro Leu Pro Asn Tyr Ile Leu Gln			
500	505	510	
Glu Ile Asp Tyr Pro Ser Arg Phe Asn Asp Leu Ala Ser Ser Leu Leu			
515	520	525	
Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys Ala Asp Arg Ala Arg Gly			
530	535	540	
Glu Glu Ala Ser Ala Ile Ser Cys Tyr Met Lys Asp His Pro Gly Ser			
545	550	555	560

Thr Glu Glu Asp Ala Leu Asn His Ile Asn Val Met Ile Ser Asp Ala
565 570 575

Ile Arg Glu Leu Asn Trp Glu Leu Leu Arg Pro Asp Ser Lys Ser Pro
580 585 590

Ile Ser Ser Lys Lys His Ala Phe Asp Ile Thr Arg Ala Phe His His
595 600 605

Leu Tyr Lys Tyr Arg Asp Gly Tyr Thr Val Ala Ser Ser Glu Thr Lys
610 615 620

Asn Leu Val Met Lys Thr Val Leu Glu Pro Val Ala Leu
625 630 635

<210> 70

<211> 696

<212> DNA

<213> Abies grandis

<400> 70

gcatttaaga gatgggatcc gtctgccaca gatttgcttc cagagtatat gaaagggttg 60
tacatggtgg tttacgaaac cgtaaatgaa attgctcgag aggcagacaa gtctcaaggc 120
cgagagacgc tcaacgatgc tcgacgagct tgggaggcct atcttgattc gtatatgaaa 180
gaagctgagt gatatctccag tggttatctg ccaacgtttg aggagtagat ggagaccagc 240
aaagtttagtt ttggttatcg catattcgca ttgcaaccca tcctcaactat ggatgttccc 300
cttactcacc acatcctgca ggaaatagac tttccattga ggttaatga cttaatatgt 360
tccatccttc gactaaaaaa tgacactcgc tgctacaagg cggacaggc ccgtggagaa 420
gaagcttcgt gtatatcgtg ttatatgaaa gagaatcctg gatcaacaga ggaagatgct 480
atcaatcata tcaacgctat ggtcaataac ttaatcaaag aagtgaattt ggagcttctc 540
cgacaggacg gcaccgctca tattgcttc aagaaacacg ctttgacat cctcaaagg 600
tcccttcacg gctacaaata ccgagatggg ttcagcgttg ccaacaagga aaccaagaat 660
tgggtgagga gaacagtctt tgagtctgtg cctttg 696

<210> 71

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<220>

<221> misc_feature

<222> (1)..(20)

<223> Reverse RACE primer 10-2

<400> 71
acgaagcttc ttctccacgg

20

<210> 72
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(20)
<223> Reverse RACE primer 10-4

<400> 72
ggatcccatc tcttaactgc

20

<210> 73
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(27)
<223> PCR primer AP1

<400> 73
ccatcctaat acgactcact ataggc

27

<210> 74
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(23)
<223> PCR primer AP2

<400> 74
actcaactata gggctcgagc ggc

23

<210> 75
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(24)
<223> PCR primer AG9F

<400> 75
atggctttt tttctatctt gccc

24

<210> 76
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(24)
<223> PCR primer AG9R

<400> 76
ttacaaaggc acagactcaa ggac

24

<210> 77
<211> 1890
<212> DNA
<213> Abies grandis

<220>
<221> CDS
<222> (1)..(1890)

<400> 77
atg gct ctt gtt tct atc ttg ccc ttg tct tcc aaa tcg gtc ctg cac 48
Met Ala Leu Val Ser Ile Leu Pro Leu Ser Ser Lys Ser Val Leu His
1 5 10 15

aaa tcg tgg atc gtt tct act tat gag cat aag gct atc agt aga aca 96
Lys Ser Trp Ile Val Ser Thr Tyr Glu His Lys Ala Ile Ser Arg Thr
20 25 30

atc cca aat ctt gga ttg cgt ggg cga ggg aaa tct gtg aca cat tcc 144
Ile Pro Asn Leu Gly Leu Arg Gly Arg Gly Lys Ser Val Thr His Ser
35 40 45

ctg aga atg agt ttg agc acc gca gtc tct gat gat cat ggt gta caa 192
Leu Arg Met Ser Leu Ser Thr Ala Val Ser Asp Asp His Gly Val Gln
50 55 60

aga cgc ata gtc gag ttt cat tcc aat ctg tgg gac gac gat ttc ata 240

Arg Arg Ile Val Glu Phe His Ser Asn Leu Trp Asp Asp Asp Phe Ile			
65	70	75	80
caa tct cta tca acg cct tat ggg gca cct tca tac cgt gaa cgt gct			288
Gln Ser Leu Ser Thr Pro Tyr Gly Ala Pro Ser Tyr Arg Glu Arg Ala			
85	90	95	
gat aga ctt att gtg gaa gta aag ggt ata ttc act tca att tca gcg			336
Asp Arg Leu Ile Val Glu Val Lys Gly Ile Phe Thr Ser Ile Ser Ala			
100	105	110	
gaa gat gga gaa cta atc act ccc ctc aat gat ctc att caa cgc ctt			384
Glu Asp Gly Glu Leu Ile Thr Pro Leu Asn Asp Leu Ile Gln Arg Leu			
115	120	125	
tta atg gtc gat aac gtt gaa cgt tta ggg att gat aga cat ttc aaa			432
Leu Met Val Asp Asn Val Glu Arg Leu Gly Ile Asp Arg His Phe Lys			
130	135	140	
aat gag ata aaa gca gca cta gac tat gtt tac agt tat tgg aac gaa			480
Asn Glu Ile Lys Ala Ala Leu Asp Tyr Val Tyr Ser Tyr Trp Asn Glu			
145	150	155	160
aaa ggc att ggc agt gga agt gat agt ggt gtt gct gat ctc aac tca			528
Lys Gly Ile Gly Ser Gly Ser Asp Ser Gly Val Ala Asp Leu Asn Ser			
165	170	175	
act gcc ctg ggg ttt cga att ctt cga cta cac gga tac agt gtt tct			576
Thr Ala Leu Gly Phe Arg Ile Leu Arg Leu His Gly Tyr Ser Val Ser			
180	185	190	
tca gat gtg ttg gaa cac ttc aaa gag gag aag gag aag ggg cag ttt			624
Ser Asp Val Leu Glu His Phe Lys Glu Glu Lys Glu Lys Gly Gln Phe			
195	200	205	
gta tgt tcg gcc atc caa aca gag gaa gag ata aaa agc gtt ctg aat			672
Val Cys Ser Ala Ile Gln Thr Glu Glu Glu Ile Lys Ser Val Leu Asn			
210	215	220	
tta ttt cgg gcc tcc ctc att gcc ttt cct ggg gag aaa gtt atg gaa			720
Leu Phe Arg Ala Ser Leu Ile Ala Phe Pro Gly Glu Lys Val Met Glu			
225	230	235	240
gag gct gaa atc ttc tct aaa ata tat tta aaa gaa gcc tta caa aat			768
Glu Ala Glu Ile Phe Ser Lys Ile Tyr Leu Lys Glu Ala Leu Gln Asn			
245	250	255	
att gct gtc tcc agt ctt tca cga gag ata gag tac gtt ctg gag gat			816
Ile Ala Val Ser Ser Leu Ser Arg Glu Ile Glu Tyr Val Leu Glu Asp			
260	265	270	
ggt tgg caa aca aat atg cca aga ttg gaa aca agg aac tac atc gat			864
Gly Trp Gln Thr Asn Met Pro Arg Leu Glu Thr Arg Asn Tyr Ile Asp			
275	280	285	
gta ttg gga gag aac gat cgt gat gag acg tta tat atg aac atg gag			912
Val Leu Gly Glu Asn Asp Arg Asp Glu Thr Leu Tyr Met Asn Met Glu			
290	295	300	
aaa ctt tta gaa att gca aaa ttg gag ttc aat att ttt cac tcc tta			960
Lys Leu Leu Glu Ile Ala Lys Leu Glu Phe Asn Ile Phe His Ser Leu			

305	310	315	320	
caa cag aga gag cta aaa gac ctc tcc aga tgg tgg aaa gat tcg ggt Gln Gln Arg Glu Leu Lys Asp Leu Ser Arg Trp Trp Lys Asp Ser Gly				1008
325		330	335	
tcc tct cac ctg aca ttt tct cgg cat cgt cat gtg gaa ttc tac gct Phe Ser His Leu Thr Phe Ser Arg His Arg His Val Glu Phe Tyr Ala				1056
340	345		350	
ctg gca tct tgc att gaa act gat cgc aaa cat tcc gga ttc aga ctc Leu Ala Ser Cys Ile Glu Thr Asp Arg Lys His Ser Gly Phe Arg Leu				1104
355	360	365		
ggc ttt gcc aaa atg tgt cat ctt atc acg gtt ttg gac gat ata tac Gly Phe Ala Lys Met Cys His Leu Ile Thr Val Leu Asp Asp Ile Tyr				1152
370	375	380		
gac acc ttt gga aca atg gag gag ctg gaa ctc ttc act gca gca ttt Asp Thr Phe Gly Thr Met Glu Glu Leu Glu Leu Phe Thr Ala Ala Phe				1200
385	390	395	400	
aag aga tgg gat ccg tct gcc aca gat ttg ctt cca gag tat atg aaa Lys Arg Trp Asp Pro Ser Ala Thr Asp Leu Leu Pro Glu Tyr Met Lys				1248
405	410		415	
ggg ttg tac atg gtg gtt tac gaa acc gta aat gaa att gct cga gag Gly Leu Tyr Met Val Val Tyr Glu Thr Val Asn Glu Ile Ala Arg Glu				1296
420	425	430		
gca gac aag tct caa ggc cga gag acg ctc aac gat gct cga cga gct Ala Asp Lys Ser Gln Gly Arg Glu Thr Leu Asn Asp Ala Arg Arg Ala				1344
435	440	445		
tgg gag gcc tat ctt gat tcg tat atg aaa gaa gct gag tgg atc tcc Trp Glu Ala Tyr Leu Asp Ser Tyr Met Lys Glu Ala Glu Trp Ile Ser				1392
450	455	460		
agt ggt tat ctg cca acg ttt gag gag tac atg gag acc agc aaa gtt Ser Gly Tyr Leu Pro Thr Phe Glu Glu Tyr Met Glu Thr Ser Lys Val				1440
465	470	475	480	
agt ttt ggt tat cgc ata ttc gca ttg caa ccc atc ctc act atg gat Ser Phe Gly Tyr Arg Ile Phe Ala Leu Gln Pro Ile Leu Thr Met Asp				1488
485	490	495		
gtt ccc ctt act cac cac atc ctg cag gaa ata gac ttt cca ttg agg Val Pro Leu Thr His His Ile Leu Gln Glu Ile Asp Phe Pro Leu Arg				1536
500	505	510		
ttt aat gac tta ata tgt tcc atc ctt cga ctt aaa aat gac act cgc Phe Asn Asp Leu Ile Cys Ser Ile Leu Arg Leu Lys Asn Asp Thr Arg				1584
515	520	525		
tgc tac aag gcg gac agg gcc cgt gga gaa gaa gct tcg tgt ata tcg Cys Tyr Lys Ala Asp Arg Ala Arg Gly Glu Glu Ala Ser Cys Ile Ser				1632
530	535	540		
tgt tat atg aaa gag aat cct gga tca aca gag gaa gat gct atc aat Cys Tyr Met Lys Glu Asn Pro Gly Ser Thr Glu Glu Asp Ala Ile Asn				1680
545	550	555	560	

cat atc aac gct atg gtc aat aac tta atc aaa gaa gtg aat tgg gag 1728
His Ile Asn Ala Met Val Asn Asn Leu Ile Lys Glu Val Asn Trp Glu
565 570 575

ctt ctc cga cag ggc acc gct cat att gct tgc aag aaa cac gct 1776
Leu Leu Arg Gln Asp Gly Thr Ala His Ile Ala Cys Lys Lys His Ala
580 585 590

ttt gac atc ctc aaa ggt tcc ctt cac ggc tac aaa tac cga gat ggg 1824
Phe Asp Ile Leu Lys Gly Ser Leu His Gly Tyr Lys Tyr Arg Asp Gly
595 600 605

ttc agc gtt gcc aac aag gaa acc aag aat tgg gtg agg aga aca gtc 1872
Phe Ser Val Ala Asn Lys Glu Thr Lys Asn Trp Val Arg Arg Thr Val
610 615 620

ctt gag tct gtg cct ttg 1890
Leu Glu Ser Val Pro Leu
625 630

<210> 78

<211> 630

<212> PRT

<213> Abies grandis

<400> 78

Met Ala Leu Val Ser Ile Leu Pro Leu Ser Ser Lys Ser Val Leu His
1 5 10 15

Lys Ser Trp Ile Val Ser Thr Tyr Glu His Lys Ala Ile Ser Arg Thr
20 25 30

Ile Pro Asn Leu Gly Leu Arg Gly Arg Gly Lys Ser Val Thr His Ser
35 40 45

Leu Arg Met Ser Leu Ser Thr Ala Val Ser Asp Asp His Gly Val Gln
50 55 60

Arg Arg Ile Val Glu Phe His Ser Asn Leu Trp Asp Asp Asp Phe Ile
65 70 75 80

Gln Ser Leu Ser Thr Pro Tyr Gly Ala Pro Ser Tyr Arg Glu Arg Ala
85 90 95

Asp Arg Leu Ile Val Glu Val Lys Gly Ile Phe Thr Ser Ile Ser Ala
100 105 110

Glu Asp Gly Glu Leu Ile Thr Pro Leu Asn Asp Leu Ile Gln Arg Leu
115 120 125

Leu Met Val Asp Asn Val Glu Arg Leu Gly Ile Asp Arg His Phe Lys
130 135 140

Asn Glu Ile Lys Ala Ala Leu Asp Tyr Val Tyr Ser Tyr Trp Asn Glu
145 150 155 160

Lys Gly Ile Gly Ser Gly Ser Asp Ser Gly Val Ala Asp Leu Asn Ser
165 170 175

Thr Ala Leu Gly Phe Arg Ile Leu Arg Leu His Gly Tyr Ser Val Ser
180 185 190

Ser Asp Val Leu Glu His Phe Lys Glu Glu Lys Glu Lys Gly Gln Phe
195 200 205

Val Cys Ser Ala Ile Gln Thr Glu Glu Glu Ile Lys Ser Val Leu Asn
210 215 220

Leu Phe Arg Ala Ser Leu Ile Ala Phe Pro Gly Glu Lys Val Met Glu
225 230 235 240

Glu Ala Glu Ile Phe Ser Lys Ile Tyr Leu Lys Glu Ala Leu Gln Asn
245 250 255

Ile Ala Val Ser Ser Leu Ser Arg Glu Ile Glu Tyr Val Leu Glu Asp
260 265 270

Gly Trp Gln Thr Asn Met Pro Arg Leu Glu Thr Arg Asn Tyr Ile Asp
275 280 285

Val Leu Gly Glu Asn Asp Arg Asp Glu Thr Leu Tyr Met Asn Met Glu
290 295 300

Lys Leu Leu Glu Ile Ala Lys Leu Glu Phe Asn Ile Phe His Ser Leu
305 310 315 320

Gln Gln Arg Glu Leu Lys Asp Leu Ser Arg Trp Trp Lys Asp Ser Gly
325 330 335

Phe Ser His Leu Thr Phe Ser Arg His Arg His Val Glu Phe Tyr Ala
340 345 350

Leu Ala Ser Cys Ile Glu Thr Asp Arg Lys His Ser Gly Phe Arg Leu
355 360 365

Gly Phe Ala Lys Met Cys His Leu Ile Thr Val Leu Asp Asp Ile Tyr
370 375 380

Asp Thr Phe Gly Thr Met Glu Glu Leu Glu Leu Phe Thr Ala Ala Phe
385 390 395 400

Lys Arg Trp Asp Pro Ser Ala Thr Asp Leu Leu Pro Glu Tyr Met Lys
405 410 415

Gly Leu Tyr Met Val Val Tyr Glu Thr Val Asn Glu Ile Ala Arg Glu
420 425 430

Ala Asp Lys Ser Gln Gly Arg Glu Thr Leu Asn Asp Ala Arg Arg Ala
435 440 445

Trp Glu Ala Tyr Leu Asp Ser Tyr Met Lys Glu Ala Glu Trp Ile Ser
450 455 460

Ser Gly Tyr Leu Pro Thr Phe Glu Glu Tyr Met Glu Thr Ser Lys Val
465 470 475 480

Ser Phe Gly Tyr Arg Ile Phe Ala Leu Gln Pro Ile Leu Thr Met Asp
485 490 495

Val Pro Leu Thr His His Ile Leu Gln Glu Ile Asp Phe Pro Leu Arg

500

505

510

Phe Asn Asp Leu Ile Cys Ser Ile Leu Arg Leu Lys Asn Asp Thr Arg
515 520 525

Cys Tyr Lys Ala Asp Arg Ala Arg Gly Glu Glu Ala Ser Cys Ile Ser
530 535 540

Cys Tyr Met Lys Glu Asn Pro Gly Ser Thr Glu Glu Asp Ala Ile Asn
545 550 555 560

His Ile Asn Ala Met Val Asn Asn Leu Ile Lys Glu Val Asn Trp Glu
565 570 575

Leu Leu Arg Gln Asp Gly Thr Ala His Ile Ala Cys Lys Lys His Ala
580 585 590

Phe Asp Ile Leu Lys Gly Ser Leu His Gly Tyr Lys Tyr Arg Asp Gly
595 600 605

Phe Ser Val Ala Asn Lys Glu Thr Lys Asn Trp Val Arg Arg Thr Val
610 615 620

Leu Glu Ser Val Pro Leu
625 630

<210> 79

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<220>

<221> misc_feature

<222> (1)..(30)

<223> Mutagenesis primer 6eBamHIF

<400> 79

caattaagag atgggacccg tccgcgtatgg

30

<210> 80

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<220>

<221> misc_feature

<222> (1)..(30)

<223> Mutagenesis primer 6eBamHIR

<400> 80

ccatcgcgaa cgggtcccat ctcttaattg

30

<210> 81
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(30)
<223> Mutagenesis primer 9eBamHIF

<400> 81
gcatttaaga gatgggaccc gtctgccaca 30

<210> 82
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
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<222> (1)..(30)
<223> Mutagenesis primer 9eBamHIR

<400> 82
ctgtggcaga cgggtcccat ctcttaaatg 30

<210> 83
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<223> Mutagenesis primer 732eNdeIF

<400> 83
cgagatgcca tacgtgaata cgca 25

<210> 84
<211> 25
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<400> 84
ctgcgtattc acgtatggca tctcg

25

<210> 85
<211> 30
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<222> (1)..(30)
<223> PCR primer 6-NdeI-M

<400> 85
ctgatagcaa gctcatatgg ctcttcttgc

30

<210> 86
<211> 34
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<222> (1)..(34)
<223> PCR primer 6-NdeI-R

<400> 86
gcccacgcgt ctcatatgg aatcagtaga tgcg

34

<210> 87
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<223> PCR primer 6-BamHI

<400> 87

caccatagggatcctcag ttaatattt

29

<210> 88

<211> 30

<212> DNA

<213> Artificial Sequence

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<222> (1)..(30)

<223> PCR primer 8-NdeI-M

<400> 88

taaggcgacatcatggctc tggtttcttc

30

<210> 89

<211> 29

<212> DNA

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<222> (1)..(29)

<223> PCR primer 8-BamHI

<400> 89

gcataaacgc atagcgatc ctacaccaa

29

<210> 90

<211> 30

<212> DNA

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<222> (1)..(29)

<223> PCR primer 9-NdeI-M

<400> 90

cccgggatc ggacatatgg ctcttgtttc

30

<210> 91

<211> 34
<212> DNA
<213> Artificial Sequence

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<222> (1)..(34)
<223> PCR primer 9_BamHI

<400> 91
ggtcgactct agaggatcca ctagtgatat ggat

34

<210> 92
<211> 27
<212> DNA
<213> Artificial Sequence

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<222> (1)..(27)
<223> PCR primer 11-NdeI-M

<400> 92
gaacatatatgg ctctccttgc tatcgta

27

<210> 93
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<222> (1)..(31)
<223> PCR primer 11-NdeI-R

<400> 93
ggtgtggtg tacatatgag acgcatacgg g

31

<210> 94
<211> 34
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<400> 94
gagactagac tggatcccat atacactgta atgg

34

<210> 95
<211> 24
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<222> (1)..(24)
<223> PCR primer 2-NdeI-M

<400> 95
caaaggagc acatatggct ctgg

24

<210> 96
<211> 30
<212> DNA
<213> Artificial Sequence

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<400> 96
ctgatgatgg tcataatgaga cgcataaggta

30

<210> 97
<211> 28
<212> DNA
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<222> (1)..(28)
<223> PCR primer 2-BamHI

<400> 97

gaccttatta ttatggatcc ggtagttag

28

<210> 98
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<213> Artificial Sequence

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<222> (1)..(30)
<223> PCR primer 3-NdeI-R

<400> 98
ccgatgtatgg tcatatgaga cgcattggcg

30

<210> 99
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<212> DNA
<213> Artificial Sequence

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<223> PCR primer 3-BamHI

<400> 99
gggcatacatat ttgagcggat cctacaaagg

30

<210> 100
<211> 24
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<222> (1)..(24)
<223> Mutagenesis primer 3elBamHIF

<400> 100
cgtttggaa tccatagaca tttc

24

<210> 101
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<220>
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<222> (1)..(24)
<223> Mutagenesis primer 3e1BamHIR

<400> 101
gaaatgtcta tggattccca aacg

24

<210> 102
<211> 26
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<220>
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<222> (1)..(26)
<223> PCR primer 3e2BamHIF

<400> 102
gaagagatgg gaccgtcct cgatag

26

<210> 103
<211> 26
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<213> Artificial Sequence

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<220>
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<222> (1)..(26)
<223> Mutagenesis primer 3e2BamHIR

<400> 103
ctatcgagga cgggtcccat ctcttc

26

<210> 104
<211> 25
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<222> (1)..(25)
<223> Mutagenesis primer 3e1NdeIF

<400> 104
gaacacgaag tcctatgtga agagc

25

<210> 105
<211> 25
<212> DNA
<213> Artificial Sequence

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<220>
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<222> (1)..(25)
<223> Mutagenesis primer 3e1NdeIR

<400> 105
gctttcaca taggacttcg tgttc

25

<210> 106
<211> 25
<212> DNA
<213> Artificial Sequence

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<222> (1)..(25)
<223> Mutagenesis primer 3e3NdeIF

<400> 106
gatacgctca cttatgctcg ggaag

25

<210> 107
<211> 25
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<221> misc_feature
<222> (1)..(25)
<223> Mutagenesis primer 3e2NdeIR

<400> 107
cttccccgagc ataagtgagc gtatc

25